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<p>(21) International Application Number: PCT/US99/16747</p> <p>(22) International Filing Date: 23 July 1999 (23.07.99)</p> <p>(30) Priority Data:</p> <table border="0"> <tr> <td>60/093,859</td> <td>23 July 1998 (23.07.98)</td> <td>US</td> </tr> <tr> <td>60/101,825</td> <td>25 September 1998 (25.09.98)</td> <td>US</td> </tr> <tr> <td>60/102,960</td> <td>2 October 1998 (02.10.98)</td> <td>US</td> </tr> <tr> <td>60/108,184</td> <td>12 November 1998 (12.11.98)</td> <td>US</td> </tr> <tr> <td>60/123,675</td> <td>9 March 1999 (09.03.99)</td> <td>US</td> </tr> </table> <p>(71) Applicants (for all designated States except US): YEDA RESEARCH AND DEVELOPMENT CO., LTD [IL/IL]; P.O. Box 95, 76100 Rehovot (IL). PRESIDENT AND FELLOWS OF HARVARD COLLEGE [US/US]; Suite 727, Holyoke Center, 1350 Massachusetts Avenue, Cambridge, MA 02138 (US).</p> <p>(72) Inventors; and</p> <p>(75) Inventors/Applicants (for US only): AHARONI, Rina [IL/IL]; Hess Street 24B, 76346 Rehovot (IL). TEITELBAUM, Dvora [IL/IL]; Shkolnik Street 5, 76209 Rehovot (IL). ARNON, Ruth [IL/IL]; Meonot Shine 9, 76100 Rehovot (IL). SELA, Michael [IL/IL]; Meonot Wix 2, 76100 Rehovot (IL). FRIDKIS-HARELI, Masha [IL/US]; 7 Divinity Avenue, Cambridge, MA 02138 (US). STROMINGER,</p>		60/093,859	23 July 1998 (23.07.98)	US	60/101,825	25 September 1998 (25.09.98)	US	60/102,960	2 October 1998 (02.10.98)	US	60/108,184	12 November 1998 (12.11.98)	US	60/123,675	9 March 1999 (09.03.99)	US	<p>Jack, L. [US/US]; 2030 Massachusetts Avenue, Lexington, MA 02173 (US).</p> <p>(74) Agent: WHITE, John, P.; Cooper & Dunham LLP, 1185 Avenue of the Americas, New York, NY 10036 (US).</p> <p>(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p> <p>Published With international search report.</p>
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<p>(54) Title: TREATMENT OF AUTOIMMUNE CONDITIONS WITH COPOLYMER 1 AND RELATED COPOLYMERS AND PEPTIDES</p> <p>(57) Abstract</p> <p>The present invention is directed to polypeptides and peptides containing at least three amino acids randomly joined in a linear array; wherein at least one of the three amino acids is an aromatic amino acid, at least one of the three amino acids is a charged amino acid and at least one amino acid is an aliphatic amino acid. In a preferred embodiment the polypeptide contains three or four of the following amino acids: tyrosine, alanine, glutamic acid or lysine. According to the present invention, the present polypeptides bind to antigen presenting cells, purified human lymphocyte antigens (HLA) and/or Copolymer 1-specific T cells. Moreover, according to the present invention, these polypeptides can be formulated into pharmaceutical compositions for treating autoimmune disease. The present invention further contemplates methods of treating an autoimmune disease in a mammal by administering a pharmaceutically effective amount of any one of the present polypeptides or peptides to the mammal.</p>																	

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Treatment of Autoimmune Conditions with Copolymer 1 and Related Copolymers and Peptides

RELATED APPLICATIONS

The present application claims the benefit of provisional applications 60/093,859 filed July 23, 1998, 60/101,825, filed September 25, 1998, 60/102,960, filed October 2, 1998, 60/106,350, filed October 30, 1998, 60/108,184, filed November 12, 1998, and 60/123,675, filed March 9, 1999, all of which are incorporated by reference herein.

GOVERNMENT FUNDING

This invention was made in part with government support under grant CA47554 awarded by the National Institutes of Health. The government has certain rights in the invention.

INTRODUCTION

The present invention provides compositions and methods for treating autoimmune diseases using therapeutically effective amounts of a peptide or polypeptide related to Copolymer 1. Copolymer 1 is a heterogeneous mixture of synthetic random linear copolymers of tyrosine, alanine, glutamic acid and lysine and, in appropriate therapeutic amounts and average molecular sizes, is used to treat multiple sclerosis. When such mixtures of synthetic random linear copolymers consist essentially of the three of the four amino acids found in Copolymer 1, they are referred to as Terpolymers. The present invention relates in part to Terpolymers. Preferably, the Terpolymers are composed of tyrosine, alanine and lysine, or of glutamic acid, tyrosine and lysine, or of glutamic acid, alanine and lysine. Surprisingly, the Terpolymers have efficacy for treating a variety of auto-immune diseases and bind to Class II major histocompatibility complex (MHC) molecules as well as to antigen presenting cells.

The present invention also includes certain peptides, comprising the four amino acids of Copolymer 1, which have also been found to have efficacy for treating a variety of autoimmune diseases and bind to Class II major histocompatibility complex (MHC) molecules as well as to antigen presenting cells. Such peptides are referred to below as "Copeptides," to stress their relationship to Copolymer 1.

BACKGROUND OF THE INVENTION

Autoimmune diseases occur when an organism's immune system fails to recognize some of the organism's own tissues as "self" and attacks them as "foreign." Normally, self-tolerance is developed early by developmental events within the immune system that prevent the organism's own T cells and B cells from reacting with the organism's own tissues. MHC cell surface proteins help regulate these early immune responses by binding to and presenting processed peptides to T cells.

This self-tolerance process breaks down when autoimmune diseases develop. Now the organism's own tissues and proteins are recognized as "autoantigens" and are attacked by the organism's immune system. For example, multiple sclerosis is believed to be an autoimmune disease occurring when the immune system attacks the myelin sheath, whose function is to insulate and protect nerves. It is a progressive disease characterized by demyelination, followed by neuronal and motor function loss. Rheumatoid arthritis ("RA") is also believed to be an autoimmune disease which involves chronic inflammation of the synovial joints and infiltration by activated T cells, macrophages and plasma cells, leading to a progressive destruction of the articular cartilage. It is the most severe form of joint disease. The nature of the autoantigen(s) attacked in rheumatoid arthritis is poorly understood, although collagen type II is a candidate.

A tendency to develop multiple sclerosis and rheumatoid arthritis is inherited – these diseases occur more frequently in individuals carrying one or more

characteristic MHC class II alleles. For example, inherited susceptibility for rheumatoid arthritis is strongly associated with the MHC class II DRB1 *0401, DRB 1 *0404, or DRB 1*0405 or the DRB1*0101 alleles. The histocompatibility locus antigens (HLA) are found on the surface of cells and help determine the individuality of tissues from different persons. Genes for histocompatibility locus antigens are located in the same region of chromosome 6 as the major histocompatibility complex (MHC). The MHC region expresses a number of distinctive classes of molecules in various cells of the body, the genes being, in order of sequence along the chromosome, the Class I, II and III MHC genes. The Class I genes consist of HLA genes, which are further subdivided into A, B and C subregions. The Class II genes are subdivided into the DR, DQ and DP subregions. The MHC-DR molecules are the best known; these occur on the surfaces of antigen presenting cells such as macrophages, dendritic cells of lymphoid tissue and epidermal cells. The Class III MHC products are expressed in various components of the complement system, as well as in some non-immune related cells.

A number of therapeutic agents have been developed to treat autoimmune diseases, including steroidal and non-steroidal anti-inflammatory drugs, for example, methotrexate; various interferons; and certain inhibitors of prostaglandin synthesis. However, these agents can be toxic when used for more than short periods of time or cause undesirable side effects. Other therapeutic agents bind to and/or inhibit the inflammatory activity of tumor necrosis factor (TNF), for example, anti-TNF specific antibodies or antibody fragments, or a soluble form of the TNF receptor. These agents target a protein on the surface of a T cell and generally prevent interaction with an antigen presenting cell (APC). However, therapeutic compositions containing natural folded proteins are often difficult to produce, formulate, store, and deliver. Moreover, the innate heterogeneity of the immune system can limit the effectiveness of drugs and complicate long-term treatment of autoimmune diseases.

Thus in order to effectively treat autoimmune diseases and other immune conditions, new drugs are needed that do not have the side effects of the present therapeutic agents and which adequately address to the innate heterogeneity of the

immune system.

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SUMMARY OF THE INVENTION

Surprisingly, Copolymer 1 and the Terpolymers and Copeptides of the present invention can be used to treat a variety of autoimmune diseases in a heterogeneous patient population. These Terpolymers and Copeptides can inhibit some of the physiological responses of T cells that attack self-antigens as these diseases progress. Moreover, Copolymer 1 and the Terpolymers and Copeptides of the present invention bind with high affinity to antigen presenting cells from different genetic backgrounds and to several class II MHC molecules to block immune cell recognition and attack. In addition, the Terpolymers and Copeptides can stimulate the growth and functioning of Copolymer 1-specific T cells to further treat and prevent various autoimmune diseases.

Accordingly, the present invention provides a composition having a polypeptide comprising three different amino acids selected from the group of amino acids comprising Copolymer 1, that is, glutamic acid, alanine, lysine, and tyrosine, in the approximate relative molar ratios found in Copolymer 1.

The present invention is also directed to peptides comprising three different amino acids selected from the group of amino acids comprising Copolymer 1,

The present invention is also directed to pharmaceutical compositions which include a therapeutically effective amount of a Terpolymer consisting essentially of amino acids tyrosine, alanine and lysine, in the molar ratio of from about 0.005 to about 0.25 tyrosine, from about 0.3 to about 0.6 alanine, and from about 0.1 to about 0.5 lysine. and a pharmaceutically acceptable carrier. This Terpolymer is preferably substantially free of glutamic acid.

The present invention further provides a pharmaceutical composition which includes a therapeutically effective amount of a Terpolymer consisting essentially of glutamic acid, tyrosine and lysine, in the molar ratio of from about 0.005 to about 0.300 glutamic acid, from about 0.005 to about 0.250 tyrosine; and from about 0.3 to about 0.7 lysine, and a pharmaceutically acceptable carrier. The Terpolymer is preferably substantially free of alanine.

The present invention is also directed to pharmaceutical compositions which

include a therapeutically effective amount of a Terpolymer consisting essentially of amino acids tyrosine, glutamic acid and alanine in the molar ratio of from about 0.005 to about 0.25 tyrosine, from about 0.005 to about 0.3 glutamic acid, and from about 0.005 to about 0.8 lysine and a pharmaceutically acceptable carrier. This Terpolymer is preferably substantially free of lysine.

The present invention also provides a pharmaceutical composition which includes a therapeutically effective amount of a Terpolymer consisting essentially of glutamic acid, alanine and lysine, in the molar ratio of from about 0.005 to about 0.3 glutamic acid, from about 0.005 to about 0.6 alanine; and from about 0.2 to about 0.7 lysine and a pharmaceutically acceptable carrier. This Terpolymer is preferably substantially free of tyrosine.

The present invention also provides a pharmaceutical composition to treat autoimmune diseases which includes a therapeutically effective amount of Copolymer 1 or a polypeptide consisting essentially of glutamic acid, alanine, tyrosine and lysine, and a pharmaceutically acceptable carrier.

The present invention further provides methods for treating and preventing autoimmune diseases in a mammal which include administering a therapeutically effective amount of a composition comprising Copolymer 1, a Terpolymer or a Copeptide. In another embodiment, the method for treating autoimmune diseases in a mammal further involves inhibiting proliferation of T cells involved in the immune attack. In another embodiment, the method for treating autoimmune diseases in a mammal involves binding the Terpolymer or Copeptide to an antigen presenting cell. In yet another embodiment, the method for treating autoimmune disease in a mammal involves binding the Terpolymer or Copeptide to a major histocompatibility complex class II protein which is associated with autoimmune diseases.

Autoimmune diseases contemplated by the present invention include arthritic conditions, demyelinating diseases and inflammatory diseases. For example, autoimmune diseases which can be treated by the present compositions include multiple sclerosis, autoimmune hemolytic anemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crone's disease, chronic immune

thrombocytopenic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis, or systemic lupus erythematosus. The present compositions can be used to treat one or more of these diseases.

BRIEF DESCRIPTION OF THE DRAWINGS

As used below

"GAL" is a random terpolymer of glutamic acid, alanine and lysine;

"TGA" or "YEA" is a random terpolymer of tyrosine, glutamic acid, and alanine;

"TAL" or "YAK" is a random terpolymer of tyrosine, alanine, and lysine;

"GTL" or "YEK" is a random terpolymer of glutamic acid, tyrosine, and lysine;
and

"YEA" is Copolymer 1.

Figure 1 illustrates the effect of Copolymer 1 and Terpolymers on proliferation of T cells which are specific for certain myelin basic protein (MBP) peptides. Several of the present Terpolymers inhibit proliferation of T cell lines which are specific for myelin basic protein antigen, MBP 84-102 (SEQ ID NO: 1). The following symbols were used: Copolymer 1 (●); GAL (□); TGA (Δ); TAL (○); GTL (X). Figure 1A illustrates inhibition of the proliferation of mouse T cell clone MBP-sp-1 specific to MBP 84-102 peptide (0.5 g/well). As a control, proliferation of mouse T cell clone MBP-sp-1 stimulated by MBP 84-102 (SEQ ID NO: 1) without inhibitor was 21,145 cpm. Figure 1B illustrates inhibition of the response of human T cell clone GP-25 to MBP 84-102 peptide (0.125 g/well). Proliferation of human T cell clone GP-25 stimulated by MBP 84-102 (SEQ ID NO: 1) peptide without inhibitor was 11,442 cpm.

Figure 2A compares binding of the present polypeptides with the binding of Copolymer 1, to Class II major histocompatibility molecules DR1 (top), DR2 (middle)

and DR4 (bottom). Binding by Copolymer 1 (■), was compared to binding by the following biotinylated Terpolymers: GAL (□); TGA (▲); GTL (Δ); and TAL (◆). The amount of Class II major histocompatibility molecule was held constant at 0.5 μg/sample and the concentration of polypeptide was varied between 0-8 μM as indicated on the y-axis. Binding was at pH 5.0 for 40 hr at 37°C. Binding was detected by capturing the polypeptide-class II complexes with an LB3.1 antibody and detecting the amount of biotinylated polypeptide bound by monitoring the absorbency at 410 nm after reaction with streptavidin-conjugated alkaline phosphatase.

Figure 2B provides Lineweaver-Burke plots of the binding data provided in Figure 2A.

Figure 3 illustrates the competitive inhibition of Copolymer 1 binding to Class II major histocompatibility molecules by the present polypeptides. Purified HLA-DR1 (top), HLA-DR2 (middle) and HLA-DR4 (bottom) molecules were incubated with a constant amount (1.5 μM) of biotinylated Copolymer 1, either alone or in the presence of one of the following unlabeled polypeptides: Copolymer 1 (■); GAL (□); TGA (▲); GTL (Δ); and TAL (◆). Inhibition by these polypeptides was compared to inhibition by the myelin basic protein antigen HA 306-318 (O) (SEQ ID NO: 2). Binding was at pH 5.0 for 40 hr at 37°C. The amount of unlabeled polypeptide was varied between 0.1 -1000 μM, as indicated on the y-axis. Specific binding is expressed as the percentage of inhibition using equation 1:

$$\text{percent inhibition} = 100 - \frac{(\text{signal with competitor} - \text{background})}{(\text{signal without competitor} - \text{background})} \times 100 \quad 1$$

Figure 4A illustrates the competitive inhibition of TAL binding to Class II major histocompatibility molecules by bacterial superantigens SEA, SEB and TSST-1. Purified HLA-DR1 (top), HLA-DR2 (middle) and HLA-DR4 (bottom) molecules were incubated with a constant amount of biotinylated TAL, in the presence of increasing amounts of unlabeled bacterial superantigen SEA (□); SEB (■); or TSST-1 (●). Binding was at pH 5.0 for 40 hr at 37°C. The amount of superantigen

was varied between 0.1 -1000 μ M, as indicated on the y-axis. Specific binding is expressed as the percentage of inhibition using equation 1.

Figure 4B illustrates the competitive inhibition of TGA binding to Class II major histocompatibility molecules by bacterial superantigens SEA, SEB and TSST-1. Purified HLA-DR1 (top), HLA-DR2 (middle) and HLA-DR4 (bottom) molecules were incubated with a constant amount of biotinylated polypeptide TGA, in the presence of increasing amounts of unlabeled bacterial superantigen SEA (\square); SEB (\blacksquare); or TSST-1 (\bullet). Binding was at pH 5.0 for 40 hr at 37°C. The amount of superantigen was varied between 0.1 -1000 μ M, as indicated on the y-axis. Specific binding is expressed as the percentage of inhibition, calculated according to equation above 1.

Figure 4C illustrates the competitive inhibition of GAL binding to Class II major histocompatibility molecules by bacterial superantigens SEA, SEB and TSST-1. Purified HLA-DR1 (top), and HLA-DR2 (bottom) molecules were incubated with a constant amount of biotinylated GAL, in the presence of increasing amounts of unlabeled bacterial superantigen SEA (\square); SEB (\blacksquare); or TSST-1 (\bullet). Binding was at pH 5.0 for 40 hr at 37°C. The amount of superantigen was varied between 0.1 -1000 μ M, as indicated on the y-axis. Specific binding is expressed as the percentage of inhibition using equation 1 above.

Figure 5 shows inhibition of binding of labeled molecules to MHC class II purified proteins by Terpolymers of the present invention. Fig. 5A shows inhibition of binding to the MHC HLA-DR1 protein. Fig. 5B shows inhibition of binding to the MHC HLA-DR4 protein. Unlabeled competitors include Terpolymers of the present invention, influenza virus hemagglutinin (HA) peptide 306-318 (SEQ ID NO:2), and type II collagen (CII) peptide 261-273 (SEQ ID NO:3). The concentration of unlabeled competitor is indicated on the abscissa. In each panel, inhibition by CII 261-273 (SEQ ID NO:3) is shown as open circles (\circ), inhibition by HA 306-318 (SEQ ID NO: 2) is shown by solid circles (\bullet), inhibition by one of the present terpolymers is indicated as shown by open or solid triangles or squares. The extent of inhibition by GTL is shown using open triangles (Δ), by TAL is shown as solid triangles (\blacktriangle), by

TGA as open squares (\square), and by Copolymer 1 as solid squares (\blacksquare). Specific binding observed and shown on the ordinate was calculated as percentage of inhibition using equation 1 above.

Figure 6 shows inhibition of IL-2 production by DR1-restricted-CII-specific T cell hybridomas in the presence of different polypeptides of the present invention. Irradiated L57.23 cells (fibroblasts transfected with a gene encoding HLA-DR1) were coincubated in duplicate with collagen peptide CII 261-273 (40 μ g/ml) and varying concentrations, shown on the abscissa, of one of the present polypeptides for 2 hr at 37°C, then T cells (clone 3.19 or 19.3 as indicated) were added, and the mixtures were further incubated for 24 hr at 37°C. Supernatants (30 μ l) were then removed, and were assayed for activation by IL-2-induced proliferation of IL-2-dependent cytotoxic T lymphocytes (CTL-L). The extent of inhibition by TAL is shown as solid circles (\bullet), by TGA as solid triangles (\blacktriangle), by GTL as open triangles (Δ), and by Copolymer 1 as solid squares (\blacksquare). Percent inhibition of CTL-L proliferation shown on the ordinate was calculated according to equation 1.

Figure 7 shows inhibition of IL-2 production by DR4-restricted CII-specific T cell hybridomas (3838 and D3) in the presence of different polypeptides of the present invention. Fig. 7A shows the effects of coincubating irradiated 3838 or D3 Priess cells with collagen peptide CII 261-273 (SEQ ID NO: 3) at the fixed concentration of 40 μ g/ml, and with varying concentrations of each of the present polypeptides, for 2 hr at 37°C. Fig. 7B shows the effects of incubating L cells transfected with a gene encoding HIA-DR4 with collagen peptide CII 261-273 (SEQ ID NO:3) at the fixed concentration of 40 μ g/ml, and with varying concentrations of each of the present polypeptides, for 2 hr at 37°C. T cells were then added (clones 3838 or D3 as indicated), samples were further incubated for 24 hr at 37°C, and supernatants were assayed as described in Figure 6. Each polypeptide was tested in duplicate. The concentration of the present polypeptides is indicated on the abscissa. The same symbols as used in Figure 6 are used for this figure.

DETAILED DESCRIPTION OF THE INVENTION

According to the present invention, polypeptides and peptides having at least three different amino acids randomly polymerized in a linear configuration are useful for treating autoimmune diseases. Autoimmune diseases occur when the immune system inappropriately attacks certain tissues or cells. The polypeptides and peptides of the present invention can prevent the immune system from attacking, for example, by suppressing the proliferation or function of T or B cells responsible for the attack, or by shielding the tissue from attack by binding to a MHC protein on the surface of the cells that make up the tissue.

Amino acids of the present invention include, but are not limited to the 20 commonly occurring amino acids. Also included are naturally occurring and synthetic derivatives, for example, selenocysteine. Amino acids further include amino acid analogs. An amino acid "analog" is chemically related forms of the amino acid having a different configuration, for example, an isomer, or a D-configuration rather than an L-configuration, or an organic molecule with the approximate size and shape of the amino acid, or an amino acid with modification to the atoms that are involved in the peptide bond, so as to be protease resistant when polymerized in a peptide or polypeptide.

The phrases "amino acid" and "amino acid sequence" as defined here and in the claims can include one or more components which are amino acid derivatives and/or amino acid analogs comprising part or the entirety of the residues for any one or more of the 20 naturally occurring amino acids indicated by that sequence. For example, in an amino acid sequence having one or more tyrosine residues, a portion of one or more of those residues can be substituted with homotyrosine. Further, an amino acid sequence having one or more non-peptide or peptidomimetic bonds between two adjacent residues, is included within this definition.

The one letter and three letter amino acid codes (and the amino acid that each represents) are as follows: A means ala (alanine); C means cys (cysteine); D means asp (aspartic acid); E means glu (glutamic acid); F means phe (phenylalanine); G means gly (glycine); H means his (histidine); I means ile

(isoleucine); K means lys (lysine); L means leu (leucine); M means met (methionine); N means asn (asparagine); P means pro (proline); Q means gln (glutamine); R means arg (arginine); S means ser (serine); T means thr (threonine); V means val (valine); W means trp (tryptophan); and Y means tyr (tyrosine).

The term "hydrophobic" amino acid is defined here and in the claims as including aliphatic amino acids alanine (A, or ala), glycine (G, or gly), isoleucine (I, or ile), leucine (L, or leu), proline (P, or pro), and valine (V, or val), the terms in parentheses being the one letter and three letter standard code abbreviations for each amino acid, and aromatic amino acids tryptophan (W, or trp), phenylalanine (F or phe), and tyrosine (Y, or tyr). The amino acids confer hydrophobicity as a function of the length of aliphatic and size of aromatic side chains, when found as residues within a protein.

The term "charged" amino acid is defined here and in the claims as including an amino acids aspartic acid (D, or asp), glutamic acid (E, or glu), histidine (H, or his), arginine (R, or arg) and lysine (K, or lys), which confer a positive (his, lys and arg) or negative (asp and glu) charge at physiological values of pH in aqueous solutions on proteins containing these residues.

Polypeptide Compositions Contemplated by the Invention

The polypeptides and peptides of the present invention comprise Copolymer 1 and Terpolymers consisting essentially of three of the four amino acids of Copolymer 1, namely tyrosine, glutamic acid, alanine and lysine. However, one of skill in the art can readily substitute structurally-related and/or charge-related amino acids without deviating from the spirit of the invention. Thus, the present invention further contemplates conservative amino acid substitutions for tyrosine, glutamic acid, alanine and lysine in the present polypeptides. Such conservative substitutions are structurally-related amino acid substitutions, including those amino acids which have about the same charge, hydrophobicity and size as tyrosine, glutamic acid, alanine or lysine. For example, lysine is structurally-related to arginine and histidine; glutamic acid is structurally-related to aspartic acid; tyrosine is structurally-related to

serine, threonine, phenylalanine and tryptophan; and alanine is structurally-related to valine, leucine and isoleucine. These and other conservative substitutions, such as structurally-related synthetic amino acids, are contemplated by the present invention.

Moreover, the Terpolymers and Copeptides can be composed of *L*- or *D*-amino acids. As is known by one of skill in the art, *L*-amino acids occur in most natural proteins. However, *D*-amino acids are commercially available and can be substituted for some or all of the amino acids used to make the Terpolymers and Copeptides. The present invention contemplates Terpolymers and Copeptides formed from mixtures of *D*- and *L*-amino acids, as well as Terpolymers and Copeptides consistently essentially of either *L*- or *D*-amino acids.

The average molecular weight and the average molar fraction of the amino acids in the Terpolymers can vary. However, an average molecular weight range of about 2,000 to about 40,000 daltons is contemplated. A preferred average molecular weight range is from about 4,000 to about 12,000 daltons. The Copeptides can be from about 7 to about 100 amino acids in length, or from about 7 to about 50 amino acids in length, or from about 7 to about 25 amino acids in length, or from about 7 to about 15 amino acids in length. Preferred average molecular weight ranges and processes of making the Terpolymers are described in U.S. Patent No. 5,800,808, which is hereby incorporated by reference in its entirety.

In one embodiment, the present invention provides Terpolymers containing tyrosine, alanine and lysine. The average molar fraction of the amino acids in these Terpolymers can vary, for example, tyrosine can be present in a mole fraction of about 0.005 to about 0.250; alanine can be present in a mole fraction of about 0.3 to about 0.6; and lysine can be present in a mole fraction of about 0.1 to about 0.5. The average molecular weight is between 2,000 to about 40,000 daltons and preferably between about 3,000 to about 35,000 daltons. In a more preferred embodiment, the average molecular weight is about 5,000 to about 25,000 daltons.

In another embodiment, the present invention provides Terpolymers containing tyrosine, glutamic acid and lysine. The average molar fraction of the amino acids in these polypeptides can also vary, for example, glutamic acid can be

present in a mole fraction of about 0.005 to about 0.300, tyrosine can be present in a mole fraction of about 0.005 to about 0.250; lysine can be present in a mole fraction of about 0.3 to about 0.7. The average molecular weight is between 2,000 to about 40,000 daltons and preferably between about 3,000 to about 35,000 daltons. In a more preferred embodiment, the average molecular weight is about 5,000 to about 25,000 daltons.

In another embodiment, the present invention provides Terpolymers containing glutamic acid, alanine and lysine. The average molar fraction of the amino acids in these polypeptides can also vary, for example, glutamic acid can be present in a mole fraction of about 0.005 to about 0.300, alanine can be present in a mole fraction of about 0.005 to about 0.600; lysine can be present in a mole fraction of about 0.2 to about 0.7. The average molecular weight is between 2,000 to about 40,000 daltons and preferably between about 3,000 to about 35,000 daltons. In a more preferred embodiment, the average molecular weight is about 5,000 to about 25,000 daltons.

In another embodiment, the present invention provides Terpolymers containing tyrosine, glutamic acid and alanine. The average molar fraction of the amino acids in these polypeptides can also vary, for example, tyrosine can be present in a mole fraction of about 0.005 to about 0.250; glutamic acid can be present in a mole fraction of about 0.005 to about 0.300; and alanine can be present in a mole fraction of about 0.005 to about 0.800. The average molecular weight is between 2,000 to about 40,000 daltons and preferably between about 3,000 to about 35,000 daltons. In a more preferred embodiment, the average molecular weight is about 5,000 to about 25,000 daltons.

In a more preferred embodiment, the mole fraction of amino acids of the Terpolymers is about what is preferred for Copolymer 1. The mole fraction of amino acids in Copolymer 1 is glutamic acid (about 0.14), alanine (about 0.43), tyrosine (about 0.10) and lysine (about 0.34). The most preferred average molecular weight for Copolymer 1 is between about 5,000 and about 9,000 daltons.

The molar ratios of the monomers of the more preferred terpolymer of

glutamic acid, alanine and tyrosine is about 0.21 to about 0.65 to about 0.14.

The molar ratios of the monomers of the more preferred terpolymer of glutamic acid, alanine and lysine is about 0.15 to about 0.48 to about 0.36.

The molar ratios of the monomers of the more preferred terpolymer of glutamic acid, tyrosine, and lysine is about 0.26 to about 0.16 to about 0.58.

The molar ratios of the monomers of the more preferred terpolymer of tyrosine, alanine and lysine is about 0.10 to about 0.54 to about 0.35.

In one embodiment, the Terpolymers and Copeptides of the present invention are capable of binding to an MHC class II protein which, preferably, is associated with an autoimmune disease. Any available method can be used to ascertain whether the Terpolymer or Copeptide binds to one or more MHC class II proteins. For example, the polypeptide can be labeled with a reporter molecule (such as a radionuclide or biotin), mixed with a crude or pure preparation of MHC class II protein and binding is detected if the reporter molecule adheres to the MHC class II protein after removal of the unbound polypeptide.

In another embodiment, the Terpolymers and Copeptides of the invention are capable of binding to an MHC class II protein associated with multiple sclerosis. A polypeptide of this embodiment can have similar or greater affinity for the antigen binding groove of an MHC class II protein associated with multiple sclerosis than does Copolymer 1. Hence, the contemplated polypeptide can inhibit binding of or displace the binding of myelin autoantigens from the MHC class II protein. One MHC class II protein associated with multiple sclerosis is HLA-DR4 (DRB1*1501).

In another embodiment, Copolymer 1, the Terpolymers and Copeptides of the invention are capable of binding to an MHC class II protein associated with an arthritic condition, for example, rheumatoid arthritis or osteoarthritis. Copolymer 1 a Terpolymer or Copeptide of this embodiment can have a greater affinity for the antigen binding groove of an MHC class II protein associated with the autoimmune disease than does a type II collagen 261-273 (SEQ ID NO:3) peptide. Hence, the contemplated Copolymer 1, Terpolymers or Copeptides can inhibit binding of or displace the type II collagen 261-273 peptide from the antigen binding groove of an

MHC class II protein. The Class II MHC protein consists of approximately equal-sized α and β subunits, both of which are transmembrane proteins. A peptide-binding cleft is formed by parts of the amino termini of both α and β subunits. This peptide-binding cleft is the site of presentation of the antigen to T cells. There are at least three types of Class II MHC molecules: HLA-DR, HLA-DQ, and HLA-DP molecules. There are also numerous alleles encoding each type of these HLA molecules. The Class II MHC molecules are expressed predominantly on the surfaces of B lymphocytes and antigen presenting cells such as macrophages.

The Copeptides of this invention are synthetic peptides at least seven amino acid residues in length and capable of binding to an MHC class II protein associated with an autoimmune disease. The Copeptide can include an amino-terminal alanine, and the sequence is selected from the group of amino acid sequences consisting of alanine - glutamic acid - lysine - tyrosine - alanine (AEKYA) (SEQ ID NO: 4); alanine - glutamic acid - lysine - valine - alanine (AEKVA) (SEQ ID NO: 5); alanine - glutamic acid - lysine - phenylalanine - alanine (AEKFA) (SEQ ID NO: 6); lysine - glutamic acid - tyrosine - alanine (KEYA) (SEQ ID NO: 7); lysine - tyrosine - alanine - glutamic acid (KYAE) (SEQ ID NO: 8); lysine - glutamic acid - valine - alanine (KEVA) (SEQ ID NO: 9); lysine - valine - alanine - glutamic acid (KVAE) (SEQ ID NO: 10); lysine - glutamic acid - phenylalanine - alanine (KEFA) (SEQ ID NO: 11); lysine - phenylalanine - alanine - glutamic acid (KFAE) (SEQ ID NO: 12); lysine - tyrosine - alanine - alanine (KYAA) (SEQ ID NO: 13); lysine - lysine - tyrosine - alanine (KKYA) (SEQ ID NO: 14); lysine - valine - alanine - alanine (KVAA) (SEQ ID NO: 15); lysine - lysine - valine - alanine (KKVA) (SEQ ID NO: 16); lysine - phenylalanine - alanine - alanine (KFAA) (SEQ ID NO: 17); and lysine - lysine - phenylalanine - alanine (KKFA) (SEQ ID NO: 18). In this embodiment, the peptide can further comprise two alanine residues, and the sequence can be selected from the group or sequences consisting of alanine - lysine - tyrosine - alanine - glutamic acid (AKYAE) (SEQ ID NO: 19); glutamic acid - alanine - lysine - tyrosine - alanine (EAKYA) (SEQ ID NO: 20); alanine - lysine - valine - alanine - glutamic acid (AKVAE) (SEQ ID NO: 21); glutamic acid - alanine - lysine - valine - alanine (EAKVA) (SEQ ID NO: 22); alanine - lysine -

phenylalanine - alanine - glutamic acid (AKFAE)(SEQ ID NO: 23); and glutamic acid - alanine - lysine - phenylalanine - alanine (EAKFA)(SEQ ID NO: 24).

In another embodiment, the polypeptide is a Copeptide which has a sequence selected from the group consisting of:

AKEYAAAAAAKAAAA (SEQ ID NO: 25)
AAEYAAAAAAKAAAA (SEQ ID NO: 26)
AAKYAEAAAAKAAAA (SEQ ID NO: 27)
EAKYAAAAAAKAAAA (SEQ ID NO: 28)
AEKYAAAAAAKAAAA (SEQ ID NO: 29)
KEAYAAAAAAKAAAA (SEQ ID NO: 30)
AEEYAAAAAAKAAAA (SEQ ID NO: 31)
EKAYAAAAAAKAAAA (SEQ ID NO: 32)
AAKYEAAAAAAKAAAA (SEQ ID NO: 33)
EAAYAAAAAAKAAAA (SEQ ID NO: 34)
EKKYAAAAAAKAAAA (SEQ ID NO: 35)
AKKYEAAAAAAAAA (SEQ ID NO: 36)
AAEYKAAAAAAAAA (SEQ ID NO: 37)
AAKYEAAAAAAAAA (SEQ ID NO: 38)
AAKYAEAAAAAAAAA (SEQ ID NO: 39)
AEYAKAAAAAAAAA (SEQ ID NO: 40)
AEKAYAAAAAAAAA (SEQ ID NO: 41)
AYKAEAAAAAAAAA (SEQ ID NO: 42) and
AKYAEAAAAAAAAA (SEQ ID NO: 43),

wherein the peptide has high affinity for an MHC class II protein.

Yet another embodiment of the invention is a Copeptide having any of the preceding sequences in which the tyrosine (Y) has been substituted by valine (F) or phenylalanine (F).

Another embodiment of the invention provides a Copeptide with an amino acid sequence capable of inhibiting the immune response to an autoantigen in a mammal, wherein the identity and position of at least one amino acid in the

polypeptide sequence corresponds to the identity and position of at least one amino acid in the peptide binding groove of an MHC class II protein. (In this embodiment, the Copeptide can contain other amino acids as indicated below). For treating multiple sclerosis or rheumatoid arthritis, the MHC class II protein can be selected from the group consisting of an HLA-DR1 protein, an HLA-DR4 protein or an HLA-DR2 protein. In a preferred embodiment, the identity and position of at least one amino acid in the polypeptide corresponds to the identity and position of an amino acid in the P1 pocket of the MHC class II peptide binding groove. More preferably, the Copeptide has a tyrosine, a valine, or a phenylalanine corresponding to the position of the P1 pocket of the MHC class II peptide binding groove. This embodiment further provides an Copeptide composition wherein the amino acid residue corresponding to the first amino acid of the P1 pocket in the MHC class II peptide binding groove is alanine. The embodiment further provides a peptide, wherein the amino acid which corresponds to the eighth amino acid of the P1 pocket in the MHC class II peptide binding groove is lysine or alanine, and the amino acid residue that corresponds to the P1 pocket is tyrosine, valine, or phenylalanine.

Another example of this invention provides a composition containing a first Copeptide and a second Copeptide wherein the first Copeptide has a lysine and the second Copeptide has an alanine at the amino acid position corresponding to the eighth amino acid beyond the P1 pocket in the MHC class II peptide binding groove.

The present Terpolymers and Copeptides can be formulated into pharmaceutical compositions containing a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, sweeteners and the like. The pharmaceutically acceptable carriers may be prepared from a wide range of materials including, but not limited to, flavoring agents, sweetening agents and miscellaneous materials such as buffers and absorbents that may be needed in order to prepare a particular therapeutic composition. The use of such media and agents with pharmaceutically active substances is well known in the art. Except insofar as any conventional

media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The present compositions may be formulated as an injectable solution or suspension, a spray solution or a suspension.

Therapeutic Methods Contemplated by the Invention

The present invention further provides methods for treating and preventing autoimmune diseases in a mammal which include administering a therapeutically effective amount of a composition having a polypeptide containing at least three different amino acids selected from the group consisting of the amino acids which comprise Copolymer 1, namely glutamic acid, tyrosine, lysine, and alanine, wherein the selected amino acids are randomly polymerized in a linear configuration. In one embodiment the polypeptide is Copolymer 1 or a Terpolymer.

Autoimmune diseases contemplated by the present invention include either cell-mediated disease (e.g. T-cell) or antibody-mediated (e.g. B cell) disorders. Such disorders can be *inter alia* arthritic conditions, demyelinating diseases and inflammatory diseases. For example, autoimmune diseases which can be treated by the present polypeptides include multiple sclerosis, autoimmune hemolytic anemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis, or systemic lupus erythematosus. The present compositions can be used to treat one or more of these diseases.

The term "arthritic condition" as used herein is a condition wherein at least one symptom of rheumatoid arthritis is observed in at least one joint of a mammal, for example in a shoulder, knee, hip, backbone or a digit of the mammal. Examples of arthritic conditions include "Polyarthritis", which is an arthritic condition that affects more than a single joint; "juvenile arthritis", an arthritic condition of humans under the

age of 21; and Felty's syndrome, which can include the symptoms of neutropenia, splenomegaly, weight loss, anemia, lymphadenopathy, and pigment spots on the skin.

In one embodiment, any autoimmune disease can be treated by the present polypeptides so long as the contemplated polypeptide binds to an MHC class II protein that has been associated with the autoimmune disease. One aspect of this embodiment provides a method which includes selecting a polypeptide that inhibits binding of an antigenic peptide to an MHC class II protein, for example, a method wherein step (a) further comprises selecting the heteropolymer that inhibits class II-specific T cell responses to an MHC class II protein-peptide complex, and a method wherein the antigenic peptide is associated with an autoimmune disease; in another embodiment of the invention, a method is provided wherein the MHC class II protein is associated with an autoimmune disease.

In another embodiment, the method for treating an autoimmune disease in a mammal further involves inhibiting the proliferation or function of T cells which are responsive to an autoantigen. RA is a T cell-mediated autoimmune disease which can be treated with the present polypeptides. The pathological process of autoimmune diseases and immune rejection is mediated by T cells. Upon binding to and recognition of an antigen, T cells proliferate, secrete cytokines and recruit additional inflammatory and cytotoxic cells to the site. The present polypeptides prevent T cell proliferation and T cell functions such as cytokine secretion and recruitment of inflammatory and cytotoxic cells to the site. When the autoimmune disease is an arthritic condition the autoantigen can be collagen, and the present polypeptides can inhibit the proliferation and function of collagen-responsive T cells.

In another embodiment, the method for treating an autoimmune disease in a mammal involves binding the polypeptide to an antigen presenting cell such as a macrophage, a dendritic cell of the lymphoid tissue or an epidermal cell. The proliferation and functions of a T cell are activated when an appropriate antigen is presented to it. By binding to antigen presenting cells, the present polypeptides may block or otherwise interfere with T cell activation.

In yet another embodiment, the method for treating an autoimmune disease in a mammal involves binding the polypeptide to a major histocompatibility complex class II protein which is associated with an autoimmune disease. The Class II MHC proteins are expressed predominantly on the surfaces of B lymphocytes and antigen presenting cells such as macrophages. These Class II MHC proteins have a peptide-binding cleft which is the site at which antigenic peptides are presented to T cells. When the present polypeptides bind to a major histocompatibility complex class II protein, those polypeptides can block or otherwise interfere with antigen presentation and/or T cell activation.

In another embodiment, the method for treating an autoimmune disease in a mammal involves binding the polypeptide to Copolymer 1-reactive B cell antibodies, and/or Copolymer 1-reactive T cells. Copolymer 1-reactive $T_H2/3$ T cells facilitate the therapeutic effects of Copolymer 1. When binding to Copolymer 1-reactive T cells, the present polypeptides stimulate those T cells proliferate, secrete antiinflammatory cytokines and enhance the therapeutic benefits of treatment by the present methods. According to the present invention, the present polypeptides also bind to autoantigen-reactive antibodies which may block the antibody from attacking the target tissue, thereby helping to prevent the autoimmune disease from progressing. For example, when the present polypeptides are bound to MBP-specific antibodies, those antibodies may not bind to MBP and thereby lead to the destruction of MBP in the myelin sheath.

The present polypeptides may be administered by any convenient route. In one embodiment the present polypeptides and peptides can be administered by injection to facilitate delivery to the tissues affected by the autoimmune disease. Thus, the present peptides and polypeptides may, for example, be injected, ingested, inhaled, or topically applied. The subject polypeptides may be incorporated into a cream, solution or suspension for topical administration. The present polypeptides are preferably administered orally, topically or by injection without addition of an adjuvant.

Useful Kits of the Invention

Another embodiment of the invention, provides a kit for assaying the binding of an analyte to an MHC protein, which includes a water-soluble MHC protein which has been recombinantly produced in a non-mammalian cell, and a means for detection of the bound analyte on the MHC protein, and instructions for use. The MHC protein used in the kit is an MHC class II protein selected from the group consisting of an MHC class II HLA-DR1 protein, an MHC class II HLA-DR2 protein and an MHC class II HLA-DR4 protein. The kit can further comprise an autoantigenic peptide.

In a preferred embodiment, the MHC class II protein is produced in an invertebrate or a microbial cell, such as an insect cell or a yeast cell and is therefore devoid of bound peptide in the antigen cleft. The means for detecting binding of the analyte to the MHC protein can be any radioactive, fluorimetric, chemiluminescent, enzymatic or colorimetric means known to one of ordinary skill in the art. In a preferred embodiment, the MHC protein is a class II HLA-DR1 or HLA-DR4 protein. Further, the kit can include also an autoantigenic peptide, such as a collagen II peptide, or a peptide derived from myelin basic protein, myelin oligodendrite protein, or a peptide from some other protein implicated in an autoimmune disease.

Synthesis of the Terpolymers of the Invention

The Terpolymers can be made by any procedure available to one of skill in the art. For example, the Terpolymers can be made under condensation conditions using the desired molar fraction of amino acids in solution or by solid phase synthetic procedures. Condensation conditions include the proper temperature, pH and solvent conditions for condensing the carboxyl group of one amino acid with the amino group of another amino acid to form a peptide bond. Condensing agents, for example, dicyclohexyl-carbodiimide, can be used to facilitate the formation of the peptide bond. Blocking groups can be used to protect functional groups, such as the side chain moieties and some of the amino or carboxyl groups, against undesired side reactions.

For example, the process disclosed in U.S. Patent 3,849,550 can be used where the N-carboxyanhydrides of tyrosine, alanine, γ -benzyl glutamate and N-trifluoroacetyl-lysine are polymerized at ambient temperatures in anhydrous dioxane with diethylamine as an initiator. The γ -carboxyl group of the glutamic acid can be deblocked by hydrogen bromide in glacial acetic acid. The trifluoroacetyl groups are removed from lysine by 1 molar piperidine. One of skill in the art readily understands that the process can be adjusted to make peptides and polypeptides containing the desired amino acids, for example, only three of the four amino acids in Copolymer 1 by selectively eliminating the reactions that relate to any one of glutamic acid, alanine, tyrosine or lysine. For purposes of the application, the terms "ambient temperature" and "room temperature" mean a temperature ranging from about 20 to about 26 degrees Centigrade ($^{\circ}\text{C}$).

The average molecular weight of the Terpolymers can be adjusted during polypeptide synthesis or after the Terpolymers have been made. To adjust the average molecular weight during polypeptide synthesis, the synthetic conditions or the amounts of amino acids are adjusted so that synthesis stops when the polypeptide reaches the approximate length which is desired. After synthesis, polypeptides with the desired average molecular weight can be obtained by any available size selection procedure, for example, chromatography of the polypeptides on a molecular weight sizing column or gel, and collection of the average molecular weight ranges desired. The present polypeptides can also be partially hydrolyzed to remove high molecular weight species, for example, by acid or enzymatic hydrolysis, and then purified to remove the acid or enzymes.

In one embodiment, the present invention provides a process for preparing Terpolymers with a desired average molecular weight which includes reacting a protected polypeptide with hydrobromic acid to form polypeptide having the desired average molecular weight profile. The reaction is performed for a time and at a temperature which is predetermined by one or more test reactions. During the test reactions, the time and temperature are varied and the average molecular weight range of a given batch of test polypeptides is determined. The test conditions which

provide the optimal average molecular weight range for that batch of polypeptides are used for the batch. Thus, polypeptides having the desired average molecular weight profile, can be produced by a process which includes reacting the protected polypeptide with hydrobromic acid for a time and at a temperature predetermined by test reaction.

In a preferred embodiment, a test sample of protected polypeptide from a given batch is reacted with hydrobromic acid for about 10-50 hours at a temperature of about 20-28°C. The best conditions for that batch are determined by running several test reactions. For example, in one embodiment, the protected polypeptide is reacted with hydrobromic acid for about 17 hours at a temperature of about 26°C.

The examples which follow describe the invention in detail with respect to showing how certain specific representative embodiments thereof can be made, the materials, apparatus and process steps being understood as examples that are intended to be illustrative only. In particular, the invention is not intended to be limited to the methods, materials, conditions, process parameters, apparatus and the like specifically recited herein.

Throughout this application, various publications, patents, and patent applications have been referred to. The teachings and disclosures of these publications, patents, and patent applications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which the present invention pertains.

It is to be understood and expected that variations in the principles of invention herein disclosed may be made by one skilled in the art and it is intended that such modifications are to be included within the scope of the present invention.

EXAMPLE I

PREPARATION OF POLYPEPTIDES

Preparation of Protected Polypeptides

Protected polypeptides are prepared as described by Teitelbaum et al., using the N-carboxyanhydride (NCA) blocked amino acids tyrosine, alanine, glutamic acid and trifluoroacetyllysine dissolved in dioxane. 1 EUR. J. IMMUN. 242 (1971). The carboxylate group on glutamic acid is blocked with a benzyl (BZ) group.

The polymerization process is initiated by the addition of 0.01 - 0.02% diethylamine. The reaction mixture is stirred at room temperature for 20 hours and then poured into water. The protected polypeptide product is filtered, washed with water and dried. The removal of the γ -benzyl blocking groups from the glutamate residue is carried out by treating the protected polypeptide with 33% hydrobromic acid in glacial acetic acid at room temperature for 6-12 hours with stirring. The product is poured into excess water, filtered, washed and dried, yielding the protected polypeptide.

Preparing Polypeptides with Molecular Weight $7,000 \pm 2,000$ Da

Treatment of γ -benzyl protected polypeptides 33% HBr in acetic acid not only insures removal of the benzyl protecting group from the γ -carboxylate of the glutamate residue but also cleaves the polypeptides into smaller polypeptides.

The time needed for obtaining a polypeptide of molecular weight 7,000 \pm 2,000 daltons depends on the reaction temperature and the size of protected polypeptide. At temperatures of between 20°C to 28°C a test reaction is performed on every batch for different time periods, for example, from 10-50 hours. A curve of average molecular weight obtained over time is drawn. The time needed for obtaining molecular weight 7,000 \pm 2,000 Da is calculated from the curve and the reaction is performed on a larger scale. On average, at 26°C, the time period for obtaining a mixture of polypeptides with a molecular weight of 7,000 \pm 2,000 Da is 17 hours. The product is poured into excess water, filtered, washed and dried,

yielding a polypeptide with a desired range of average molecular weights.

Preparation of low-toxicity lysine-containing polypeptides

Protected trifluoroacetyl-polypeptide (20 g) is dispersed in 1 liter of water and 100 g piperidine is added. The mixture is stirred for 24 hours at room temperature and filtered. The solution of crude polypeptide is distributed into dialysis bags and dialyzed at 10-20°C in water until pH 8 is attained. The polypeptide solution is dialyzed in 0.3% acetic acid and then again in water until pH 5.5 to 6.0 is obtained. This solution is then concentrated and lyophilized to dryness.

Synthesis of: Molecular weight 7,600 TGA, poly[L-Tyr^{0.136}, L-Glu^{0.21}, L-Ala^{0.648}]

1) Raw Materials:

L-Ala-NCA	18.74 g
L-Tyr-NCA	6.5 g
5-BZ-L-Glu-NCA	13 g
Diethylamine	0.165 g
Dioxane	790 ml
Hbr/AcOH (33%)	480 ml
Phenol	4.8 g
Piperidine	13.2 ml
Deionized water	
Acetic acid	

2) Procedure:

L-Tyr-NCA (6.5 g) is placed in dioxane (211 ml) and heated to 60°C for 10 min, then filtered. 5-BZ-L-Glu-NCA (13 g) is placed in dioxane (226 ml) and stirred at 20-25°C for 10 min, then filtered. L-Ala-NCA (18.74 g) is placed in dioxane (350 ml) and stirred at 20-25°C for 10 min, then filtered.

A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with the solution of L-Tyr-NCA, the solution of 5-BZ-L-Glu-NCA and the solution of L-Ala-NCA.

Diethylamine (0.165 g) in dioxane (2.5 ml) is introduced to the reaction mixture and stirred at 20-25°C for 20 hours. The reaction mixture is added to deionized water (1L), filtered and dried at 60°C under vacuum. Yield - 25.8g.

A solution of phenol (4.8 g) in Hbr/AcOH (33%;480 ml) is stirred for 20 hours. A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with a solution of Hbr/AcOH, poly[5-BZ-L-Glu,L-Ala,L-LTyr] and stirred at 26±1°C for 16 hours. The reaction mixture is added to deionized water (2L) and stirred for 1 hour. The precipitate is filtered and washed with deionized water until the pH is 6. The product is dried in a circulating air oven at 40°C, for about 40 hours. Yield - 24 g.

A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with a piperidine (13.2 ml), deionized water (1200 ml), and poly[L-Glu,L-Ala,L-LTyr], then stirred at 20-25°C for 24 hours. The resulting solution is ultrafiltered through polyethersulphone membranes with a cutoff of 5000 daltons until two thirds of the original volume is removed. The original volume is restored by addition of fresh deionized water. The process is repeated 5 times, until the impurity content is less than 1% by HPLC . The resulting solution (at full volume) is acidified to pH 4.4 with acetic acid. The solution is ultrafiltered to pH 5.5-6 and the volume is reduced to one third. The resulting solution is lyophilized to dryness.

Synthesis of Molecular Weight 8850 GAL, poly[L-Glu^{0.153},L-Ala^{0.479},L-Lys^{0.365}]

1) Raw Materials

L-Ala-NCA	14 g
N6-TFA-L-Lys-NCA	22.9 g
5-BZ-L-Glu-NCA	9.8 g
Diethylamine	0.12 g
Dioxane	850 ml
Hbr/AcOH (33%)	480 ml
Phenol	4.8 g
Piperidine	13.2 ml
Deionized water	

Acetic acid

2) Procedure

N6-TFA-L-Lys-NCA (22.9 g) in dioxane (420 ml) is stirred at 20-25°C for 10 min. and filtered. 5-BZ-L-Glu-NCA (9.8 g) in dioxane (170 ml) is stirred at 20-25°C for 10 min. and filtered. L-Ala-NCA (14 g) in dioxane (260 ml) is stirred at 20-25°C for 10 min. and filtered. A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with the solution of N6-TFA-L-Lys-NCA, the solution of 5-BZ-L-Glu-NCA and the solution of L-Ala-NCA. Diethylamine (0.12 g) in dioxane (2.5 ml) is added, and the reaction mixture is stirred at 20-25°C for 20 hours. The reaction mixture is added to deionized water (1L), filtered and dried at 60°C under vacuum.

A solution of phenol (4.8 g) in Hbr/AcOH (33%;480 ml) is stirred for 20 hours. A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with a solution of Hbr/AcOH, poly[5-BZ-L-Glu,L-Ala,N6-TFA-L-Lys] (24 g) and is stirred at 26±1°C for 16 hours. The reaction mixture is added to deionized water (2L) and stirred for 1 hour. The precipitate is filtered and washed with deionized water until pH=6. The product is dried in a circulating air oven at 40°C, about 40 hours.

A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with piperidine (13.2 ml), deionized water (1200 ml) and poly[L-Glu,L-Ala,N6-TFA-L-Lys] (24 g) is stirred at 20-25°C for 24 hours. The solution is ultrafiltered through polyethersulphone membranes with a cut off of 5000 daltons until two thirds of the original volume are removed. The original volume is restored by addition of fresh deionized water. The process is repeated 5 times, until the impurity content is less than 1% (by HPLC). The resulting solution (at full volume) is acidified to pH 4.4 with acetic acid. The solution is ultrafiltered until the pH is 5.5-6 and the volume is reduced to one third. The resulting solution is lyophilized to dryness.

Synthesis of Molecular Weight 11,050 TGL, poly[L-Tyr^{0.162}, L-Glu^{0.259},L-Lys^{0.579}]

1) Raw Materials

5-BZ-L-Glu-NCA	10.34 g
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N6-TFA-L-Lys-NCA	24.16 g
L-Tyr-NCA	5.2 g
Diethylamine	0.095 g
Dioxane	810 ml
Hbr/AcOH (33%)	460 ml
Phenol	4.6 g
Piperidine	150 ml
Deionized water	
Acetic acid	

2) Procedure

L-Tyr-NCA (5.2 g) in dioxane (180 ml) is heated to 60°C for 10 min, and filtered. N6-TFA-L-Lys-NCA (24.16 g) in dioxane (450 ml) is stirred at 20-25°C for 10 min. and filtered. 5-BZ-L-Glu-NCA (10.35 g) in dioxane (180 ml) is stirred at 20-25°C for 10 min. and filtered.

A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with the solution of N6-TFA-L-Lys-NCA, the solution of L-Tyr-NCA and the solution of 5-BZ-L-Glu-NCA. Diethylamine (0.095 g) in dioxane (2.5 ml) is introduced, and the reaction mixture is stirred at 20-25°C for 20 hours. The reaction mixture is added to deionized water (0.7L), filtered and dried at 60°C under vacuum.

A solution of phenol (4.6 g) in Hbr/AcOH (33%;460 ml) is stirred for 20 hours. A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with the solution of HB/r/AcOH and the poly[5-BZ-L-Glu,L-Tyr,N6-TFA-L-Lys]. This mixture is stirred at 26±1°C for 16 hours and then the mixture is added to deionized water (1.5 L) and stirred for ½ hour. The precipitate is filtered and washed with deionized water until the pH is 5.5.

A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with a piperidine (150 ml), deionized water (1400 ml), and poly[L-Glu,L-Tyr,N6-TFA-L-Lys] (50 g) and is stirred at 20-25°C for 24 hours. The resulting solution of poly[L-Glu, L-Tyr, L-Lys] is ultrafiltered through polyethersulphone membranes with a cut off of

5000 daltons until two thirds of the original volume were removed. The original volume is restored by addition of fresh deionized water. The process is repeated 5 times, until the impurity content is less than 1% (by HPLC). The resulting solution (at full volume) is acidified to pH 4.2 with acetic acid. The solution is ultrafiltered to a pH of 5.5-6 and the volume is reduced to one third. The resulting solution is lyophilized to dryness.

Synthesis of Molecular Weight 20,000 TAL, poly[L-Tyr^{0.102}, L-Ala^{0.542}, L-Lys^{0.353}]

1) Raw Materials

L-Ala-NCA	14 g
N6-TFA-L-Lys-NCA	22.9 g
L-Tyr-NCA	4.9 g
Diethylamine	0.1 g
Dioxane	850 ml
Hbr/AcOH (33%)	500 ml
Phenol	5 g
Piperidine	162 ml
Deionized water	
Acetic acid	

2) Procedure

L-Tyr-NCA (4.9 g) in dioxane (170 ml) is heated to 60°C for 10 min, and filtered. N6-TFA-L-Lys-NCA (22.9 g) in dioxane (417 ml) is stirred at 20-25°C for 10 min. and filtered. L-Ala-NCA (14 g) in dioxane (260 ml) is stirred at 20-25°C for 10 min. and filtered.

A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with the solution of N6-TFA-L-Lys-NCA, the solution of Tyr-NCA in dioxane and the solution of L-Ala-NCA. Diethylamine (0.1 g) in dioxane (2 ml) is introduced and the mixture is stirred at 20-25°C for 20 hours. The reaction mixture is then added to deionized water (1L), filtered and dried at 60°C under vacuum.

A solution of phenol (5 g) in HBr/AcOH (33%;500 ml) is stirred for 20 hours.

A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with the solution of HB/r/AcOH and the poly[L-Ala,L-Tyr,N6-TFA-L-Lys] and is stirred at $26\pm 1^{\circ}\text{C}$ for 16 hours. The reaction mixture is then added to deionized water (2L) and stirred for $\frac{1}{2}$ hour. The precipitate is filtered and washed with deionized water until the pH is 5.5.

A 2L Erlenmeyer equipped with a magnetic stirrer, is charged with a piperidine (162 ml), water (1500 ml) and the poly[L-Ala,L-Tyr,N6-TFA-L-Lys] (30 g), and is stirred at $20\text{--}25^{\circ}\text{C}$ for 24 hours. The resulting solution of poly[L-Ala,L-Tyr,L-Lys] is ultrafiltered through polyethersulphone membranes with a cut off of 5000 daltons until two thirds of the original volume were removed. The original volume is restored by addition of fresh deionized water. The process is repeated 5 times, until the impurity content is less than 1% (by HPLC). The resulting solution (at full volume) is acidified to pH 4.4 with acetic acid. The solution is ultrafiltered to pH 5.5-6 and the volume is reduced to one third. The resulting solution is lyophilized to dryness.

EXAMPLE 2

LOW MOLECULAR WEIGHT POLYPEPTIDES

In Vivo Tests

Three batches of copolymer-1 having an average molecular weight of 7.3 and 8.4 KDa (less than 2.5% copolymer-1 species over 40KDa) and 22KDa (more than 5% copolymer-1 species over 40KDa) were subjected to the toxicity test described below. Five mice were used in each experimental group.

Method

Copolymer-1 is dissolved in distilled water to yield a solution of 2 mg/ml of the active ingredient. Each mouse is injected with 0.5 ml of the test solution into the lateral tail vein. Mice were observed for mortality and relevant clinical signs over a 48 hour period. Observations were recorded 10 minutes, 24 hours and 48 hours

post-injection. If, at the end of 48 hours, all the animals were alive and no adverse signs had been observed, then the batch is designated "non-toxic". If, however, one or more of the mice had died or had shown adverse signs, then the batch is designated "toxic".

Results

Three of five mice died after 48 hours when treated with the 22 kDa average molecular weight Copolymer 1 polypeptides. Accordingly, this high average molecular weight batch is designated "toxic". The Copolymer 1 batches having average molecular weights of 7.3 and 8.4 kDa were both designated "non-toxic."

In Vitro Rat Basophilic Leukemia Cell Degranulation Tests

Histamine (or serotonin) release from basophile is an in vitro model for immediate hypersensitivity. The Rat Basophilic Leukemia cell line, RBL-2H_o, is uniform and easy to maintain in culture but is a highly sensitive and reproducible system for testing for degranulation. E.L. Basumian, et al., 11 EUR. J. IMMUNOL. 317 (1981). The physiological stimulus for histamine release involves binding of the antigen to membrane-bound IgE molecules, which triggers an intricate biochemical cascade. Degranulation is induced by non-IgE-mediated stimuli, including various peptides and synthetic polymers, e.g. polylysine. R.P. Siraganian, TRENDS IN PHARMACOLOGICAL SCIENCES 432 (Oct. 1983). The RBL degranulation test is, therefore, used to screen out those batches of COP-1 which evoke substantial degranulation and thus might elicit undesirable local and/or systemic side effects.

Method

Rat Basophilic Leukemia cells (RBL-2H_o), are loaded with [H³]-serotonin, followed by incubation with 100 µg of the COP-1 to be tested. Batches of COP-1 which induce non-specific degranulation, release [H³]-serotonin into the medium. The radioactivity in the medium is counted by a scintillation counter and the total radiolabeled serotonin incorporated into the cells is determined in the pelleted cells.

Percent degranulation is calculated as the percentage of serotonin released out of the total incorporated.

Results

Four batches of Copolymer 1, with average molecular weight between 8,250-14,500 were analyzed for both percentage of the species with molecular weight over 40 kDa and for degranulation of RBL's. Results are summarized in Table 1.

Table 1

Average M.W.	% of species with M.W. over 40 KDa	% Serotonin Release
6,250	< 2.5	12.4
7,300	< 2.5	21.0
13,000	> 5	66.9
14,500	> 5	67.8

As can be seen, when the percentage of high average molecular weight species is low (less than 2.5%), the percent release of serotonin is also low, and vice versa. These data indicate that lower average molecular weight Copolymer 1 polypeptides are preferable to higher average molecular weight Copolymer 1 polypeptides.

EXAMPLE 3

SUPPRESSION OF EAE BY THE POLYPEPTIDES

Injection of Copolymer 1 in incomplete Freund's adjuvant before disease induction can suppress experimental allergic encephalomyelitis (EAE). This suppression appears to be mediated by Copolymer 1-specific suppressor T cells of the T_H2 type which cross react with myelin basic protein. Lando et al., 123 J. IMMUNOL. 2156 (1979); Aharoni et al., 17 EUR. J. IMMUNOL. 23 (1993); Aharoni et al., 94 PROC. NATL. ACAD. SCI. USA 10821 (1997). Other researchers have observed

that the therapeutic effect of Copolymer 1 in multiple sclerosis patients is also associated with the induction of T_H2 cells. Lahat et al., 244 J. Neurol. 129 (1997). In this example, EAE is suppressed to by different polypeptides of the present invention.

METHODS

Copolymer 1

Copolymer 1 batches # 02095 and 55495, with average molecular weights of 6000 Da and 5800 Da, respectively, were obtained from Teva Pharmaceutical Industries (Petach Tikva, Israel).

Terpolymers

Four terpolymers were obtained from Teva Pharmaceutical Industries (Petach Tikva, Israel). The properties of these terpolymers are provided below:

1) The GAL terpolymer (SD-1689) is a mixture of polypeptides containing the following mole fraction of amino acids glutamic acid (0.153), alanine (0.479) and lysine (0.365). The range of GAL average molecular weights is about 4650 daltons to about 20,050 daltons. The average molecular weight of this GAL preparation is 8850 daltons.

2) The TGA terpolymer (SD-1690) is a mixture of polypeptides containing the following mole fraction of amino acids tyrosine (0.136), glutamic acid (0.210) and alanine (0.648). The range of TGA average molecular weights is about 1000 daltons to about 40,000 daltons. The average molecular weight of this TGA preparation is 7600 daltons.

3) The TAL terpolymer (SD-1691) is a mixture of polypeptides containing the following mole fraction of amino acids tyrosine (0.102), alanine (0.542) and lysine (0.353). The range of TAL average molecular weights is about 5700 daltons to about 34,400 daltons. The average molecular weight of this TAL preparation is about 20,000 daltons.

4) The GTL terpolymer (SD-1697) is a mixture of polypeptides containing the

following mole fraction of amino acids glutamic acid (0.259), tyrosine (0.162) and lysine (0.579). The range of GTL average molecular weights is about 4,000 daltons to about 23,500 daltons. The average molecular weight of this GTL preparation is about 11050 daltons.

A control polypeptide is used, consisting of a mixture of polypeptides containing a 1:1:1 mixture of amino acids alanine, glutamic acid and tyrosine, with an average molecular weight 26,700 Da. This polypeptide is obtained from Sigma Chemical Company (St. Louis, MO).

Induction of EAE

Two to three month old female (SJL/JxBALB/c)F1 mice are injected in all four footpads with mouse spinal cord homogenate (3.5mg/mouse) emulsified in a 1:1 ratio in complete Freund's adjuvant (CFA) supplemented with 4 mg/ml H37Ra. Pertussis toxin (0.25ml, 250ng, Sigma) is injected intravenously, immediately after and 48 hr later. Mice are examined daily from day 10 post induction for clinical signs of EAE which were scored on a 0-5 scale as described in Lando et al., 123 J. IMMUNOL. 2156 (1979).

EAE suppression by injection with incomplete adjuvant

The tested polypeptides (10mg/mouse) are injected in incomplete Freund's adjuvant (ICFA) subcutaneously in one nuchal area in 2-3 spots. EAE is induced 3 weeks later as described above.

EAE suppression by oral administration

In a second test, female Lewis rats are fed 5 mg/kg guinea pig BP or Copolymer 1 dissolved in phosphate buffered saline (PBS) at 2-3 day intervals before EAE induction. EAE is induced two days after the last feeding by injection of 25 μ g guinea pig MBP emulsified in 1:1 CFA containing 4 mg/ml mycobacterium tuberculosis (H37Ra) (Difco Lab, Detroit, Mich.). A total volume of 0.1 ml is injected into each of two hindfoot pads. Control rats are mock fed with phosphate buffered

saline.

The efficacy of orally administered Copolymer 1 for preventing EAE in rats is compared to that of rats fed guinea pig MBP by the method of Higgins et al., 140 J. IMMUNOL. 440 (1988).

Animals were examined daily from day 10 post induction for signs of disease. EAE is scored as follows: 0 = no disease; 1 = limp tail; 2 = hind limb paralysis; 3 = paralysis of all four limbs; 4 = moribund condition; and 5 = death.

RESULTS

EAE suppression by injection with incomplete adjuvant

Table 2 illustrates the effects of administering the present polypeptides by injection in ICFA prior to induction of EAE. Of the four polypeptides tested, Copolymer 1 and TAL caused the greatest EAE suppression. GTL also exhibited good suppressive activity. GAL and TGA, were somewhat less effective.

Table 2
Suppression of EAE in mice by Injection of the Present Polypeptides

Polypeptide	Incidence	MMS*	Suppression %	
			Incidence	MMS*
None (Negative Control)	11/11	4.0		
ICFA (Negative Control)	11/11	3.4	0.0	15.0
Copolymer 1 (Positive Control)	2/11	0.45	82.0	89.0
SD-1689 - GAL	7/8	3.5	12.5	12.5
SD-1690 - TGA	6/8	2.5	25.0	37.5
SD-1691 - TAL	3/8	1.1	62.5	72.5
SD-1697 - GTL	5/8	1.5	37.5	62.5
D-Copolymer 1	11/11	4.1	0.0	0.0

*MMS = Mean Maximal Score

D-Copolymer 1 is a copolymer of d-lysine, d-tyrosine, d-glutamic acid and d-alanine in the molar ratios of Copolymer 1.

Table 3 illustrates the efficacy of orally administered Copolymer 1 in

preventing the clinical manifestations of EAE in Lewis rats compared to rats receiving only phosphate buffered saline (PBS) or guinea pig basic protein (GPBP).

Table 3
Suppression of EAE in Rats by Oral Administration
of the Present Polypeptides

Fed Antigen	Incidence	MMS \pm SD	Mean Onset (days)
PBS (Control)	27/28 (96%)	1.8 \pm 0.5	11.9
GPBP	10/17 (59%) p=0.0026	0.9 \pm 0.5	11.4
Copolymer 1	13/28 (46%) p=0.00005	0.78 \pm 0.45	12.6

Each numerical value represents the cumulative results of 3-5 independent experiments. The p values represent the statistical significance of the difference from the control (PBS) group. Mean maximal score is calculated for the entire group.

These data indicate that the present polypeptides are therapeutically effective for preventing the onset and severity of EAE when administered either orally or by injection.

EXAMPLE 4

BINDING TO ANTIGEN PRESENTING CELLS

Several of the present polypeptides bind efficiently to living antigen presenting cells.

METHODS

Copolymer 1

Copolymer 1 batches # 02095 and 55495, with average molecular weights of 6000 Da and 5800 Da, respectively, were obtained from Teva Pharmaceutical Industries (Petach Tikva, Israel).

Terpolymers

GAL, TGA, TAL, GTL and control polypeptides are as described above under Example 3.

Biotinylation of antigens

Biotinylation of Copolymer 1 and Terpolymers is performed at 0°C with biotin-*N*-hydroxysuccinimide (Sigma) according to Fridkis-Hareli et al. 91 PROC. NATL. ACAD. SCI. USA 4872 (1994).

Binding of biotinylated antigens to antigen presenting cells

The biotinylated polypeptides were examined for binding to living antigen presenting cells of mouse and human origin, using fluorescently labeled streptavidin and FACS analysis. Adherent spleen cells from (SJL/JxBALB/c)F1 mice, or EBV transformed human B cells of DR7,w I I haplotype ($1 \times 10^6/100 \mu\text{l}$), were incubated at 37°C for 20 hr. with 50 μg biotinylated Copolymer 1 or Terpolymers dissolved in 100 μl PBS containing 0.1% BSA. The cells were then incubated at 4°C for 30 min. with phycoerythrin-conjugated streptavidin (Jackson Immuno Research, West Grove, PA) at a concentration of 0.5 $\mu\text{g}/100 \mu\text{l}$ cell suspension. After each incubation the cells were washed three times with PBS containing 0.1% BSA. Thereafter, cells were analyzed by flow cytometry using FACScan (Becton-Dickinson, Mountain View, CA). For each analysis, 5000 cells were examined. Dead cells were excluded on the basis of forward and side-angle light scatter.

Epstein-Barr virus (EBV) transformed B-cell lines

EBV-transformed B-cell lines were initiated according to Teitelbaum et al., 89 PROC. NATL. ACAD. SCI. USA 137 (1992). Approximately 20×10^6 peripheral blood mononuclear cells were cultured with B95.8 cell line supernatant, for 1 hr at 37 °C. The cells were then washed and cultured in RPMI medium with 10% FCS and cyclosporin A (10 $\mu\text{g}/\text{ml}$) to deplete T cells.

RESULTS

Table 4 illustrates the binding of terpolymers and Copolymer 1 polypeptides to living antigen presenting cells, including mouse spleen macrophages and human EBV transformed B-cell lines. Data illustrating both the percent of binding and the intensity of cell staining are provided (Table 4 I+II). TAL bound the most efficiently - better even than Copolymer 1. GAL and GTL also bound very well -- the same or even somewhat better than Copolymer 1. TGA bound well but somewhat less than Copolymer 1.

TAL bound most efficiently both to spleen macrophages of (SJL/J x BALB/c) F₁ mice and to EBV-transformed B cells from a normal DR7.w11 donor, as expressed by the intensity of the binding (Table 4).

Table 4**Binding of Terpolymers to antigen presenting cells****I. Antigen presenting cells from mouse spleen macrophages**

Polypeptide	% Binding	MFI*
Copolymer 1 (positive control)	85	493
SD-1689 - GAL	88	600
SD-1690 - TGA	74	39
SD-1691 - TAL	100	1929
SD-1697 - GTL	90	973

*MFI = Mean Fluorescence Intensity

II. Antigen presenting cells from human EBV transformed B-cell line

Polypeptide	% Binding	MFI*
Copolymer 1 (positive control)	96	727
SD-1689 - GAL	95	661
SD-1690 - TGA	72	49
SD-1691 - TAL	100	1438
SD-1697 - GTL	97	1057

*MFI = Mean Fluorescence Intensity

EXAMPLE 5**THE PRESENT POLYPEPTIDES BIND
TO PURIFIED HUMAN LEUKOCYTE ANTIGENS (HLA)**

This example illustrates that polypeptides of the present invention bind to human B cells and to purified human lymphocyte antigens with high affinity, including the HLA-DR1, HLA-DR2 and HLA-DR4 molecules.

METHODS**Cell lines and antibodies**

Homozygous EBV-transformed human B lymphocyte lines used for immunoaffinity purification of HLA-DR1, -DR2 and -DR4 molecules were LG-2

(DRB1*), MGAR (DRB1*1501) and Preiss (DRB*0401/DRB4*0101), respectively.

Cells were grown in RPMI 1640 supplemented with 10% FCS, 2mM glutamine, 50 U/ml penicillin G and 50 µg/ml streptomycin in roller bottles and stored as pellets at -80°C. The anti-DR hybridoma LB3.1 (IgG2b) is grown in serum-free medium (Macrophage-SFM, Gibco BRL). See Gorga et al., 103 CELL. IMMUNOL. 160 (1986).

Protein purification

Immunoaffinity purification of HLA-DR1, -DR2 and -DR4 molecules is performed, with minor modifications, as previously reported by Gorga et al., 262 J. BIOL. CHEM. 16087 (1987). Briefly, detergent soluble membrane preparations from LG-2, MGAR and Priess cells were passed at a flow rate of approximately 11 ml/hr through a series of columns in the following sequence: Sepharose CL-6B (30 ml), normal mouse serum-Aff-gel 10 (10 ml), protein A-Sepharose CL-4B (5 ml) and LB3.1-protein A-Sepharose CL-4B (5 ml). DR2a (DRB5*0101) and Drw53 (DRB4*0101), the products of DR genes linked to the DRB1 alleles were not removed from the MGAR and Priess lysates before passage through the LB3.1 immunoaffinity column, and contaminate the DR2 and DR4 preparations in the amount of 5-10%. All the subsequent steps were as previously described by Gorga et al., 262 J. BIOL. CHEM. 16087 (1987). The eluate is dialyzed against 0.1% deoxycholate, 10 mM Tris-HCl, pH 8.0 and concentrated on a Centriprep 30 membrane (amicon). Protein concentrations were determined by bicinchonitric acid assay (Pierce Chemical Co.).

Peptides and polypeptides

Copolymer 1

Copolymer 1 batches # 55495 and 52596, with average molecular weight of 5800 daltons and 8,150 daltons, respectively, were obtained from Teva Pharmaceutical Industries (Petach Tikva, Israel). Copolymer 1 batch 52596 had a molar ratio of 1 tyrosine: 1.5 glutamic acid: 4.3 alanine: 3.1 lysine.

Myelin Basic Protein Peptides

MBP peptides were synthesized on an Applied Biosystems Peptide Synthesizer using solid phase techniques. Barany et al., THE PEPTIDES 1 (1979). Peptides purified by reversed-phase HPLC. The peptides used were HA 306-318, having the sequence PKYVKQNTLKLAT (MW 1718) (SEQ ID NO: 2), and MBP 84 102, having the sequence DENPVVHFFKNIVTPRTPP (MW 2529) (SEQ ID NO: 1).

Terpolymers

GAL, TGA, TAL, GTL and control polypeptides are as described above under Example 3.

Polypeptide labeling

Biotinylation of the various polypeptides is performed as in Example 4. Unreacted biotin is removed by dialysis (Spectra/Por® membrane MWCO 500, Spectrum Medical Industries).

Assays for polypeptide binding to class II MHC proteins

Solutions: The solutions used in this assay were the following. Binding buffer is 20 mM 2-[N-morpholino]ethanesulfonic acid (MES), 1% n-octyl β -D-glycopyranoside, 140 mM NaCl, 0.05% NaN₃, pH 5.0, unless otherwise specified. PBS is 150 mM sodium chloride, 7.5 mM sodium phosphate, dibasic, 2.5 mM sodium phosphate, monobasic, pH 7.2. TBS is 137 mM sodium chloride, 25 mM Tris pH 8.0, 2.7 mM potassium chloride. TTBS is TBS plus 0.05% Tween-20.

Microtiter Assay Plate Preparation: Ninety-six well microtiter immunoassay plates (PRO-BIND™, Falcon) were coated with 1 μ g/well affinity-purified LB3.1 monoclonal antibodies in PBS (100 μ l total) for 18 hrs at 4°C. The wells were then blocked with TBS containing 3% BSA for 1 hr at 37°C and washed three times with TTBS. Before sample addition, 50 μ l of TBS/1% BSA is added to each well.

Binding reactions: Detergent-solubilized HLA-DR1, -DR2 and -DR4 molecules (0.5 $\mu\text{g}/\text{sample}$) were incubated with biotinylated peptides at various concentrations for 40 hours at 37°C in 50 μl of the binding buffer and transferred to prepared microtiter assay plates and incubated for 1 hr at 37°C for capture of polypeptide-class II complexes.

Inhibition reactions: Biotinylated polypeptides at a final concentration of 1.5 μM in 50 μl of binding buffer were coincubated with unlabeled polypeptides as well as the peptides HA 306-318 (SEQ ID NO: 2) or MBP 84-102 (SEQ ID NO: 1), used as inhibitors, and HLA-DR molecules for 40 hr at 37°C.

Detection of class II/polypeptide complexes: Bound polypeptide-biotin is detected using streptavidin-conjugated alkaline phosphatase as follows. Plates were washed three times with TTBS and incubated with 100 μl of streptavidin-conjugated alkaline phosphatase (1:3000, BioRad) for 1 hr at 37°C, followed by addition of p-nitrophenyl phosphate in triethanolamine buffer (BioRad). The absorbency at 410 nm is monitored by a microplate reader (Dynatech MR4000).

RESULTS

Terpolymers Binding to Class II MHC Proteins

Detergent-soluble HLA-DR1, HLA-DR2 and HLA-DR4 proteins were purified from homozygous EBV-transformed B cell lines LG-2 (DRB1*0101), MGAR (DRB1*1501) and Priess (DRB1*0401), respectively, as described previously by Fridkis-Hareli et al., 160 J. IMMUNOL. 4386 (1998). Three different preparations of Copolymer 1 had bound to these molecules with high affinity. *Id.* To determine the affinity of the terpolymers for HLA-DR proteins, binding assays were carried out with biotinylated Terpolymers, and compared to Copolymer 1. The polypeptides were incubated at a range of concentrations with purified HLA-DR1, HLA-DR2 and HLA-DR4 molecules at pH 5.0 followed by capture with class II-specific mAb and

detection with alkaline phosphatase-streptavidin.

Binding by TAL and Copolymer 1 to detergent-soluble HLA-DR1 and HLA-DR4 molecules is better than that of GAL, TGA or GTL. However, GTL and Copolymer 1 bound better than the other polypeptides to HLA-DR2, based on the saturation binding curves (Fig. 2A), and on K_d values, calculated from the double-reciprocal plots of the binding data (Fig. 2B, Table 5).

Competitive binding assays were carried out with biotinylated Copolymer 1 and the following unlabeled inhibitors: Copolymer 1, TAL, TGA, GAL, TGL, MBP 84-102 and HA 306-318 polypeptides (Fig. 3). The MBP 84-102 (SEQ ID NO: 1) peptide is a poor inhibitor of the binding of Copolymer 1 to HLA-DR2. The binding of biotinylated Copolymer 1 to detergent-soluble HLA-DR1 and -DR4 molecules is efficiently inhibited by unlabeled TGA, TAL, HA 306-318 (SEQ ID NO: 2) and Copolymer 1. However, binding of biotinylated Copolymer 1 to detergent-soluble HLA-DR1 and -DR4 molecules is inhibited more than 10-fold less by TGL, as indicated by 50% inhibitory dosages (IC_{50}) (Fig. 3, Table 5). Similarly, GAL is also a poor inhibitor of Copolymer 1 binding to HLA-DR1 and -DR4 molecules. In general, the binding pattern to HLA-DR2 is similar to that observed for HLA-DR1 (Table 5). These results show that the polypeptides of three amino acids, in particular TAL and TGA bind to class II MHC molecules with an affinity range similar to that of antigenic peptides and of Copolymer 1. Hence, TAL and TGA are effective competitors for the class II MHC molecules to which Copolymer 1 binds. Based on their binding capacity, the polypeptides could be arranged in the following order:

- (A) binding to HLA-DR1: Copolymer 1 > TAL > GTL > TGA >> GAL;
- (B) binding to HLA-DR2: Copolymer 1 > GTL > TAL > GAL > TGA;
- (C) binding to HLA-DR4: TAL > Copolymer 1 >> TGA > GTL > GAL.

Table 5
Affinity of the present polypeptides
for purified human HLA-DR1, -DR2 and -DR4 molecules

Polypeptide ¹	DR1 ²		DR2		DR4	
	K _d ³	IC ₅₀ ⁴	K _d	IC ₅₀	K _d	IC ₅₀
Copolymer 1	7.4	8.8	8.2	10.1	1.5	10.8
TAL	2.0	3.3	1.7	2.7	2.0	6.5
GAL	0.5	⁵	1.7	⁵	0.3	⁵
TGA	1.0	1.3	0.8	9.5	0.8	1.0
TGL	0.4	43.0	5.0	25.4	0.8	43.0

Effect of superantigens on the binding of polypeptides to HLA-DR molecules

Bacterial superantigens SEA, SEB and TSST-1 have been shown to inhibit Copolymer 1 binding to purified HLA-DR molecules only at very high concentrations. Fridkis-Hareli et al., 160 J. IMMUNOL. 4386 (1998). To examine the effect of these superantigens on the binding of Terpolymers to purified HLA-DR1, HLA-DR2 and HLA-DR4 molecules, competitive binding assays were carried out with unlabeled

¹

Copolymer 1 polypeptides with average MW of 5,800; TAL, MW 20,000; GAL, MW 8,850; TGA, MW 7,600; and TGL, MW 11,050, were incubated at a range of concentrations with purified HLA-DR1, -DR2 and -DR4 molecules at pH 5.0 followed by capture with class II-specific mAb and peptide detection with alkaline phosphatase-streptavidin.

²

Detergent-soluble HLA-DR1, -DR2 and -DR4 molecules were purified as described in Materials and Methods.

³

K_d, the dissociation constant at equilibrium, is calculated from the slope of the double reciprocal plot (Fig. 2B), and is expressed as x 10⁻⁸ M.

⁴

IC₅₀, inhibitory concentration giving 50% inhibition, is calculated based on the competitive binding assays (Fig. 3), and is expressed as x 10⁻⁶ M.

⁵

IC₅₀ values for GAL could not be determined exactly, but were less than 1000 μM (see Fig. 3).

SEA, SEB and TSST-1.

Binding of TAL to HLA-DR1, HLA-DR2 and HLA-DR4 is only inhibited by the superantigens at high molar ratios of superantigen: for example, fifty times the amount of superantigen is needed to inhibit TAL binding (Fig. 4A). However, binding of TGA and GAL is inhibited more significantly by the superantigens (Fig. 4B and C), indicating that these polypeptides bound the HLA antigens with lower affinity.

EXAMPLE 6

INHIBITION OF MBP-INDUCED T CELL PROLIFERATION

This example illustrates that the proliferation of T cells which are normally activated by myelin basic protein (MBP) can be inhibited by simultaneous exposure to the present polypeptides.

METHODS

Copolymer 1

Copolymer 1 batches # 02095 and 55495, with average molecular weights of 6000 Da and 5800 Da, respectively, were obtained from Teva Pharmaceutical Industries (Petach Tikva, Israel).

Myelin Basic Protein Peptides which were synthesized on an Applied Biosystems Peptide Synthesizer using solid phase techniques. Barany et al., THE PEPTIDES 1 (1979). Peptides purified by reversed-phase HPLC. The peptides used were HA 306-318, having the sequence PKYVKQNTLKLAT (MW 1718)(SEQ ID NO: 2), and MBP 84 102, having the sequence DENPVVHFFKNIVTPRTPP (MW 2529) (SEQ ID NO: 1).

Terpolymers

GAL, TGA, TAL, GTL and control polypeptides are as described above under Example 3.

T cell lines and clones

Myelin Basic Protein (MBP) specific T-cell lines originated from spleens of mice which, ten days earlier, were immunized with 20 μg of the 84-102 peptide of MBP emulsified in complete Freund's adjuvant supplemented with 4 mg/ml of Mycobacterium tuberculosis H37Ra. Cells were cultured and selected *in vitro* using the immunizing antigen (0.2-1 mg/plate), in culture medium (RPMI, 2 mM glutamine, 1 mM sodium pyruvate, non essential amino acids, 5×10^{-5} M 2-mercaptoethanol, 100 /ml penicillin, 100 μg /ml streptomycin), supplemented with 1% autologous serum. After 4 days, cells were transferred to culture medium containing 10% FCS and supplemented with 10% supernatant of Con A activated normal spleen cells as T cell growth factor (TCGF). Every fourteen to twenty one days, cells were stimulated by exposure to the immunizing antigen presented on syngeneic irradiated (3000 rad) spleen cells (50×10^6 /plate) for 3 days, followed by propagation in TCGF medium. Cloning of T cell lines is performed by limiting dilution at 0.3 cells/well in microliter plate in the presence of the antigen (2-10 μg /well) and irradiated syngeneic spleen cells (5×10^6 /well).

Human T cell lines were derived from peripheral blood mononuclear cells according to Teitelbaum et al., 89 PROC. NATL. ACAD. SCI. USA 137 (1992). Approximately 5×10^6 cells were incubated in each well of a 24-well culture plate with Copolymer 1 or MBP (50 μg /ml) in culture medium supplemented with 10% heat-inactivated autologous serum. After 7 days of culture, the cells were transferred to culture medium containing 10% fetal calf serum and recombinant human interleukin 2 (20 units/ml). The cells were grown continuously in this medium with periodic exposure to antigen presented on irradiated (3000 rad), autologous mononuclear cells, every 14-18 days.

Proliferation assay

Cells of T lines or clones were tested for their specific proliferative response 10-21 days after antigenic stimulation. T Cells (1.5×10^4) were cultured in triplicates with 5×10^5 irradiated spleen cells and with the indicated antigens in a final volume of 0.2 ml in 10% FCS culture medium. At the end of 48 hr incubation, cultures were pulsed with 1 μ Ci [3 H]-thymidine (standard deviation <20% of the mean cpm), and harvested 6-12h later.

Inhibition studies

Inhibition of the T-cell proliferative response is studied by adding various concentrations of Copolymer 1 and Terpolymers plus the stimulating MBP antigen to the proliferation assay system. Inhibition is calculated as percent inhibition using equation 2:

$$\% \text{ Inhibition} = [1 - (\text{cpm with inhibitor} / \text{cpm without inhibitor})] \times 100.$$

2

RESULTS

Figure 1 illustrates how copolymer 1 and terpolymers effect the proliferation of T cells which are specific for certain myelin basic protein (MBP) peptides. In general, T cells proliferate when exposed to the antigen to which they were sensitized. Thus, MBP and, in particular, certain antigenic peptides from MBP stimulate the proliferation of MBP-specific T cells.

Copolymer 1 and Terpolymers did not stimulate proliferation of T cells which were specific for the 84-102 peptide of MBP. Instead, they significantly inhibited the proliferation of T cells exposed to this MBP antigen.

TAL exhibited the most efficient inhibition of proliferation in T cells specific for the MBP 84-102 antigen. Inhibition by TAL is even greater than that provided by Copolymer 1. TGA induced lower inhibition of T cell proliferation. GAL and GTL inhibited T cell proliferation in a dose responsive manner similar to Copolymer 1.

EXAMPLE 7**TERPOLYMERS ARE RECOGNIZED
BY SOME COPOLYMER 1-SPECIFIC T CELLS**

Terpolymers can stimulate some Copolymer 1-specific T cell lines to proliferate and secrete the cytokine, IL-4.

METHODS**Copolymer 1**

Copolymer 1 batches # 02095 and 55495, with average molecular weight of 6000 Da and 5800 Da, respectively, were obtained from Teva Pharmaceutical Industries (Petach Tikva, Israel).

Myelin Basic Protein Peptides which were synthesized on an Applied Biosystems Peptide Synthesizer using solid phase techniques. Barany et al., THE PEPTIDES 1 (1979). Peptides purified by reversed-phase HPLC. The peptides used were HA 306-318, having the sequence PKYVKQNTLKLAT (MW 1718) (SEQ ID NO: 2), and MBP 84 102, having the sequence DENPVVHFFKNIVTPRTPP (MW 2529) (SEQ ID NO: 1).

Terpolymers

GAL, TGA, TAL, GTL and control polypeptides are as described above under Example 3.

T cell lines and clones

Mouse T cell lines and clones were established according to Aharoni et al., 23 Eur. J. Immunol. 17 (1993); Aharoni et al., 94 PROC. NATL. ACAD. SCI. USA 10821 (1997). Copolymer 1 specific lines were originated from spleens of mice which, 15 to 35 days earlier, had been rendered unresponsive to EAE by subcutaneously injecting each mouse with 5-10 mg Copolymer 1, emulsified in incomplete Freund's adjuvant (Difco). Alternatively, Copolymer 1 specific lines were obtained from the

lymph nodes of mice which had been immunized ten days earlier with 200 μ g Copolymer 1 emulsified in complete Freund's adjuvant (Difco) supplemented with 4 mg/ml of Mycobacterium tuberculosis H37Ra (Difco).

Copolymer 1-specific T cell lines were used and T cell clones LN-1, LN-2, S-3, 5-22-5, C-14, and C-52. The LN-2 antibodies were derived from lymph nodes of (SJL/J x BALB/c) F₁ mice injected with Copolymer 1 in CFA. The 5-22-5 antibodies were obtained from spleens of (SJL/J x BALB/C) F₁ mice injected with Copolymer 1 in CFA, according to Aharoni et al., 23 EUR. J. IMMUNOL. 17 (1993); Aharoni et al., PROC. NATL. ACAD. SCI. USA 10821 (1997).

Human T cell clones were derived from peripheral blood mononuclear cells according Teitelbaum et al., 89 PROC. NATL. ACAD. SCI. USA 137 (1992). Approximately 5×10^6 cells were incubated in each well of a 24-well culture plate with Copolymer 1 or MBP (50 μ g/ml) in culture medium supplemented with 10% heat-inactivated autologous serum. After 7 days of culture, the cells were transferred to culture medium containing 10% fetal calf serum and recombinant human interleukin 2 (20 units/ml). The cells were grown continuously in this medium with periodic exposure to antigen presented on irradiated (3000 rad), autologous mononuclear cells, every 14-18 days. The C-52 T-cell clone was derived from a DR7,w11 donor, also according to Teitelbaum et al., 89 PROC. NATL. ACAD. SCI. USA 137 (1992).

Proliferation assay

Cells of T lines or clones were tested for their specific proliferative response 10-21 days after antigenic stimulation. T Cells (1.5×10^4) were cultured in triplicates with 5×10^5 irradiated spleen cells or with human EBV-transformed B cells (5×10^4), and with the indicated antigens in a final volume of 0.2 ml in 10% FCS culture medium. At the end of 48 hr incubation, cultures were pulsed with 1 μ Ci [3 H]-thymidine and then harvested 6-12 hr later. The variations of triplicates from their mean were under 20%.

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cell line cross-reacted only with TAL. No cell lines cross reacted with GTL or with AGT (1:1:1) which has the same amino acids as TGA but in a different mole fraction than TGA or Copolymer 1.

Table 6
Cross reactivity of Terpolymers
with Copolymer 1 for Copolymer 1 specific T-cell lines and clones

I. Murine T-cell lines and clones

T-cells Polypeptide	Cross reactivity with Copolymer 1 (%)							
	LN -3		S-3		LN-1		S-22-5	
	prol*	IL-4 [‡]	prol*	IL-4 [‡]	prol*	IL-4 [‡]	prol*	IL-4 [‡]
SD-1689 - GAL	130	139	49	11	0	1	0	0
SD-1690 - TGA	3	6	102	107	0	1	0	0
SD-1691 - TAL	3	7	2	3	64	120	0	0
SD-1697 - GTL	2	4	12	6	0	1	0	0
1:1:1 AGT	2	0	2	2	1	0	2	0T

*prol = as measured by proliferation. [‡]IL-4 = as measured by Interleukin-4.

II. Human T-cell Clones

T-cells Polypeptide	Cross reactivity with Copolymer 1 (%)	
	C-14 proliferation	C-52 proliferation
SD-1689 - GAL	4	75
SD-1690 - TGA	1	58
SD-1691 - TAL	0	0
SD-1697 - GTL	0	5

EXAMPLE 8

TERPOLYMERS CROSS-REACT WITH ANTI-COPOLYMER 1 ANTIBODIES

Antibodies directed against Copolymer 1 cross-react with Terpolymers which lack either tyrosine, glutamic acid or alanine. However, Terpolymers lacking lysine are not recognized efficiently by anti-Copolymer 1 antibodies.

Antibodies

Mouse anti-MBP and anti-Copolymer 1 monoclonal antibodies were obtained by fusion of MBP- or Copolymer 1-immunized spleen cells from SJL/J mice, with the NSO/1 murine plasmacytoma cell line. Teitelbaum et al., Proc. Natl. Acad. Sci. USA 9528 (1991).

Radioimmunoassay

Flexible plastic microtiter plates were coated with Copolymer 1 or Terpolymers (2 μ g/ml). After 16 hr incubation at room temperature, plates were washed three times and saturated for 2 hr with PBS containing 2% bovine serum albumin, 0.05% Tween 20, 0.1% sodium azide, 10 mM EDTA, and heparin at 5 units/ml ("PBS buffer"). Monoclonal antibody supernatants (50 μ l), were added to the wells for a 2 hr incubation, and the wells were washed again with PBS buffer. 125 I-labeled goat anti-mouse Fab antibodies (1 x 10⁵ cpm/well) were added for overnight incubation at 4°C. After extensive washing, radioactivity is measured in a gamma counter.

Methods

ELISA Assay for Antibody Cross-Reactivity

A standard ELISA assay is employed using anti-Copolymer 1 polyclonal antibodies and microtiter plates coated with 2 μ g/ml of terpolymer preparation.

Copolymer 1

Copolymer 1 with the following amino acid composition is obtained from Teva Pharmaceutical Industries (Petach Tikva, Israel).

<u>Amino Acid</u>	<u>Molar Fraction</u>
L-glutamic acid	0.141
L-alanine	0.427
L-tyrosine	0.095
L-lysine	0.338

Terpolymers

The four Terpolymers of Example 1 were used.

Results

Table 7 indicated that anti-Copolymer 1 polyclonal antibodies cross react with Terpolymers which lack either tyrosine, glutamic acid or alanine. The relatively high percentage binding of the terpolymers lacking glutamic acid (TAL) might be explained by its high average molecular weight. Terpolymers which lack lysine are not efficiently recognized by anti-Copolymer 1 antibodies. These data suggest that charged amino acids like lysine may play a role in the recognition and binding of Copolymer 1 and Terpolymers.

Table 7

Terpolymers	MW*	Percent Binding in separate experiments				Mean	S.D.
		1	2	3	3		
TAL	20,000	111.1	130.1	115.8	114.0	117.8	8.48
GAL	8,850	7.5	10.8	9.3	9.2	9.2	1.35
GTL	11,050	98.7	87.0	n.d.†	n.d.†	92.9	8.30
TGA	7,600	87.9	79.3	n.d.†	n.d.†	83.6	6.12

* daltons. † n.d. - not determined.

Cross reactivity of Terpolymers with Copolymer 1-reactive monoclonal antibodies

The cross reactivity of the Terpolymers with Copolymer 1 at the level of B cell

response is tested using monoclonal antibodies (mAbs), that are either reactive with both Copolymer 1 and MBP (mAbs 2-2-18 and 3-1-45), or are reactive with only Copolymer 1 (mAbs 3-3-9 and 5-7-2). See Teitelbaum et al., 88 Proc. Natl. Acad. Sci. USA 9528 (1991).

Table 8 illustrates that the Terpolymers differed in their ability to bind these mAbs. TGA and GTL were not recognized by any of the Copolymer 1 specific mAbs. On the other hand, TAL and GAL bound to Copolymer 1 and MBP specific mAbs with an affinity which is similar to that of Copolymer 1. GAL and TAL differed only in the binding to one mAb i.e. 5-7-2 which bound to TAL and not to GAL.

Table 8
Cross reactivity of Terpolymers
with MBP- and Copolymer 1-reactive B cell antibodies

Antibody Polypeptide	Cross reactivity with Copolymer 1 (%)			
	2-2-18	3-1-45	3-3-9	5-7-2
SD-1689 - GAL	96	98	107	10
SD-1690 - TGA	3	2	1	10
SD-1691 - TAL	96	98	103	106
SD-1697 - GTL	1	2	1	1

2-2-18 is anti mouse MBP monoclonal antibody **cross reactive** with Copolymer 1

3-1-45 is anti Copolymer 1 monoclonal antibody **cross reactive** with MBP

3-3-9 is anti Copolymer 1 monoclonal antibody **non cross reactive** with MBP

5-7-2 is anti Copolymer 1 monoclonal antibody **non cross reactive** with MBP

EXAMPLE 9

COPOLYMER 1 AND TERPOLYMERS COMPETE WITH COLLAGEN FOR BINDING TO HUMAN LEUKOCYTE ANTIGENS AND INHIBIT COLLAGEN- SPECIFIC T-CELL RESPONSE

This example illustrates that Copolymer 1, TAL, GAL, GTL, and TGA compete for binding to MHC proteins with the rheumatoid arthritis-associated

immunodominant collagen antigen, CII 261-273 (SEQ ID NO: 3).

Methods

Protein Expression and Purification

Recombinant HLA-DR1 and HLA-DR4 molecules (encoded by DRA/DRB I *0101 and *0401, respectively) were expressed in *Drosophila* S2 cells as described in Stern, L. et al. 68 CELL 465 (1992) and Dessen, A. et al. 7 IMMUNITY 473 (1997). Cells were grown in roller bottles at 26°C in Excell 401 medium (Sigma, St. Louis, MO) supplemented with 0-5% fetal bovine serum (Sigma). Cells were induced by addition of CuSO₄ to 1 mM final concentration, then incubated an additional 4-5 days. Immunoaffinity purification of recombinant HLA-DR1 and HLA-DR4 is performed as previously reported by Stern, L. et al. 68 CELL 465 (1992) and Dessen, A. et al. 7 IMMUNITY 473 (1997). Supernatant from harvested cells is sequentially passed through Protein A, Protein G and Protein A-LB3.1 columns, followed by elution of the bound HLA-DR with 50 mM 3-cyclohexylamino-1-propane sulfonic acid (CAPS), pH 11.5, and neutralized with 200 mM phosphate (pH 6.0). The eluate is concentrated on a Centriprep 10 membrane (Amicon). Protein concentrations were determined by bicinchoninic acid assay (Pierce Chemical Co.).

Polypeptide labeling

The present polypeptides and the HA 306-318 peptide were biotinylated as in Examples 4 and 7.

Class II MHC protein binding assay

In this assay, water-soluble recombinantly-produced proteins were incubated with biotinylated polypeptides of the present invention and varying quantities of unlabeled competitor polypeptides, collagen CII peptides or influenza virus HA peptides. Assays were performed in 96-well microliter immunoassay plates (PRO-BOND™, Falcon) which were coated with affinity-purified LB3.1 monoclonal antibodies. Antibody coating is performed by placing 100 µl of 10.0 µg/ml LB3.1

monoclonal antibodies in each well and incubating at 4°C for 18 hrs. Microtiter wells were then blocked with Tris buffered saline (TBS) containing 3% bovine serum albumin (BSA) for 1 hr at 37°C and washed three times with TTBS. Before sample addition, 50 μ l of TBS containing 1% BSA is added to each well. Phosphate buffered saline (PBS) is 150 mM sodium chloride, 7.5 mM sodium phosphate dibasic, 2.5 mM sodium phosphate monobasic, pH 7.2. Tris buffered saline (TBS) is 137 mM sodium chloride, 25 mM TRIS pH 8.0, 2.7 mM potassium chloride. TTBS is TBS with 0.05% Tween-2G. Other solutions used in this assay are described in Fridkis-Hareli, M. et al., 160 J. IMMUNOL. 4386 (1998).

Binding analysis is performed by incubating the water soluble DR molecules with biotinylated polypeptides of the present invention and varying concentrations of unlabeled inhibitors (Copolymer 1, TAL, GAL, GTL, TGA, Collagen CII 261-273 peptide or HA 306-318 peptide). The collagen type CII peptide 261-273, has SEQ ID NO: 3 (AGFKGEQGPKGEP) and a molecular weight of 1516. The concentration of DR employed is 0.15 μ M. The final concentration of biotinylated Copolymer 1 or terpolymers is 1.5 μ M. Incubation is for 40 hr at 37°C in 50 μ l binding buffer at pH 5.0.

Bound label is detected using streptavidin-conjugated alkaline phosphatase as follows. Plates were washed three times with TTBS and incubated with 100 μ l of streptavidin-conjugated alkaline phosphatase (1:3000, BioRad, Richmond, VA) for 1 hr at 37°C, followed by addition of p-nitrophenyl phosphate in triethanolamine buffer (BioRad). The absorbency at 410 nm is monitored by a microplate reader (model MR4000, Dynatech, Chantilly, VA).

T cell hybridoma and antigen presenting cell (APC) binding assays

Copolymer 1 and Terpolymers were tested to ascertain if they could inhibit activation of T cells responsive to the collagen CII peptide. Mouse DR1-restricted 3.19 and 19.3 T cell hybridomas and mouse DR4-restricted 3838 and D3 T cell hybridomas were used. Rosloniec, E. F., et al., 185 J..EXP. MED. 1113-1122 (1997); Andersson, E. C., et al., PROC. NATL. ACAD. SCI. USA (1998). Antigen presenting

cells (APCs) were L cells transfected with DR1 (the L57.23 cell line provided by Rosloniec, E. F., et al., 1997, 185 J. Exp. Med. 1113-1122 (1997)), L cells transfected with DR4, and Priess cells (DRB1*0401/DRB4*0101). T cell stimulation experiments were performed in 96-well microliter plates in a total volume of 0.2 ml. Irradiated (3000-rad) APC (2.5×10^4 /well) were coincubated with CII 261-273 ($40 \mu\text{g/ml}$) and varying concentrations of the present polypeptides for 2 hr at 37°C , then T cells (5×10^4 /well) were added and the incubation is continued for 24 hr at 37°C . Supernatants ($30 \mu\text{l}$) were removed and incubated with IL-2 dependent CTL-L (5×10^4 /well) for 12 hr, followed by labeling with ^3H -thymidine ($1 \mu\text{Ci/well}$) for 12 hr. Plates were harvested and the radioactivity is monitored using a 1450 microbeta Plus liquid scintillation counter (Wallac, Gaithersburg, MD).

RESULTS

Class II MHC protein binding assay

The recombinant water-soluble HLA-DR1 and -DR4 proteins produced in insect cells were largely free of bound autoantigens or other peptides. Hence, data obtained from insect cell produced proteins can more accurately indicate the actual binding affinities for polypeptides. Fridkis-Hareli et al., 160 J. IMMUNOL. 4386 (1998) (the entire contents of which are hereby incorporated herein by reference).

Competitive binding of each of the Copolymer 1 and Terpolymers to HLA-DR1, HLA-DR2 and HLA-DR4 molecules is depicted in Figure 5. Binding of each of the Copolymer 1 (YEA, top panel Fig. 5A) and Terpolymers is substantially greater than that of the CII 261-273 (SEQ ID NO: 3) peptide, as judged by quantity of CII 261-273 (SEQ ID NO: 3) peptide required for 50% inhibition. As also observed above, TAL bound HLA-DR1 and HLA-DR4 with greater affinity than did Copolymer 1. The kinetics of inhibition by unlabeled TAL (YAK, bottom panel Fig. 5A) polypeptides were also somewhat superior to that of the influenza virus peptide HA 306-318 (SEQ ID NO: 2). However, the influenza virus peptide HA 306-318 inhibited the binding of Copolymer 1 and of Terpolymers more efficiently than the CII 261-273 peptide.

T cell Hybridoma and antigen presenting cell binding assay results

Copolymer 1 and Terpolymers also inhibited DR1-restricted T cell activation by CII collagen peptide (Fig. 6). T cell activation was detected by observing IL-2 production by DR1-restricted-CII-specific T cell hybridomas. Collagen peptide CII 261-273 (SEQ ID NO: 3) at varying concentrations was coincubated with one of the present polypeptides and then T cells (clone 3.19 or 19.3 as indicated) were added, and the mixtures were further incubated. The supernatants from these incubated cells are removed, and were assayed for IL-2 by observing whether the supernatant induced proliferation of IL-2-dependent cytotoxic T lymphocytes (CTL-L). The extent of inhibition by TAL is shown as solid circles (●), by TGA as solid triangles (▲), by GTL as open triangles (Δ), and by Copolymer 1 as solid squares (■). Percent inhibition of CTL-L proliferation shown on the ordinate was calculated using equation 1:

Again, TAL is the most potent inhibitor. However, GTL and Copolymer 1 were also potent inhibitors of T cell activation by the CII collagen peptide. TGA inhibited activation less efficiently. Similar results were obtained with other batches of Copolymer 1 and Terpolymers.

A similar inhibition of activation of DR4-restricted T cells was observed, as shown in Figure 7. IL-2 production was used to assess activation of DR4-restricted CII-specific T cell hybridomas (3838 and D3). The presence of different polypeptides inhibited IL-2 production, indicating that they inhibited DR4-restricted T cell activation. Fig. 7A shows the effects of coincubating irradiated 3838 or D3 Priess cells with collagen peptide CII 261-273 (SEQ ID NO: 3) at the fixed concentration of 40 $\mu\text{g/ml}$, and with varying concentrations of polypeptides, for 2 hr at 37°C. Fig. 7B shows the effects of incubating L cells transfected with a gene encoding HLA-DR4 with collagen peptide CII 261-273 (SEQ ID NO: 3) at the fixed concentration of 40 $\mu\text{g/ml}$, and with varying concentrations of GAL, TAL, GTL, TGA, and Copolymer 1, for 2 hr at 37°C. T cells were then added (clones 3838 or D3 as indicated), samples were further incubated for 24 hr at 37°C. Supernatants (30 μl) were then removed, and were assayed for activation by IL-2-induced proliferation of

IL-2-dependent cytotoxic T lymphocytes (CTL-L). Each polypeptide mixture was tested in duplicate. The concentration of the present polypeptides is indicated on the abscissa. The extent of inhibition by TAL is shown as solid circles (●), by TGA as solid triangles (▲), by GTL as open triangles (Δ), and by Copolymer 1 as solid squares (■). Percent inhibition of CTL-L proliferation shown on the ordinate was calculated using equation 1.

EXAMPLE 10

COPOLYMER 1 SEQUENCE MOTIFS WHICH BIND TO HLA-DR1, HLA-DR2 AND HLA-DR4 MOLECULES

Methods

Protein Expression and Purification

Recombinant HLA-DR1 and HLA-DR4 molecules (encoded by DRA/DRB 1 *0101 and *0401, respectively) were expressed in *Drosophila* S2 cells as described in Stern, L. et al. 68 CELL 465 (1992) and Dessen, A. et al. 7 IMMUNITY 473 (1997). Cells were grown in roller bottles at 26°C in Excell 401 medium (Sigma, St. Louis, MO) supplemented with 0-5% fetal bovine serum (Sigma). Cells were induced by addition of CuSO₄ to 1 mM final concentration, then incubated an additional 4-5 days. Immunoaffinity purification of recombinant HLA-DR1 and HLA-DR4 is performed as previously reported by Stern, L. et al. 68 CELL 465 (1992) and Dessen, A. et al. 7 IMMUNITY 473 (1997). Supernatant from harvested cells is sequentially passed through Protein A, Protein G and Protein A-LB3.1 columns, followed by elution of the bound HLA-DR with 50 mM 3-cyclohexylamino-1-propane sulfonic acid (CAPS), pH 11.5, and neutralized with 200 mM phosphate (pH 6.0). The eluate is concentrated on a Centrprep 10 membrane (Amicon). Protein concentrations were determined by bicinchoninic acid assay (Pierce Chemical Co.).

Binding and Quantifying Bound Polypeptide

Copolymer 1 is incubated with water-soluble HLA-DR1, -DR2 or -DR4 molecules at a molar ratio of 1:1 for 40 hr at 37°C. Unbound Copolymer 1 is

separated from bound Copolymer 1 by Centricon ultrafiltration. Bound Copolymer 1 is then extracted from the HI-A-DR complex by acid treatment (Chicz, R. et al. 178 J. EXP. MED. 27 (1993)) and subjected to amino acid analysis.

For HPLC separation and microsequencing after elution, approximately 5-10% of the Copolymer 1 mixtures are fractionated by microbore, HPLC using a Zorbax C₁₈ 1.0 mm reverse-phase column on a Hewlett-Packard 1090 HPLC with 1040 diode array detector. At a flow rate of 54 μ l/min, Copolymer 1 is eluted with a gradient of 0.055% trifluoroacetic acid (TFA) in acetonitrile (0% at 0- 10 min, 33% at 73 min and 60% at 105 min). Strategies for peak elections, reverse phase separation and Edman microsequencing were performed as in Chicx et al. 178 J. EXP. MED. 27 (1993), and Lane, W. et al. 10 J. PROT. CHEM. 151(1991).

Structural Characterization of Bound Copolymer 1

Fractionation of Copolymer 1 bound to human HLA-DR1, HLA-DR2 or HLA-DR4 molecules from homozygous EBV-transformed B cell lines, indicated that nearly all of the bound Copolymer 1 was found in the high average molecular weight fractions and less than 10% of bound Copolymer 1 was in the lower average molecular weight fractions.

To characterize the hydrophobicity and size of Copolymer 1 bound to isolated recombinant HLA molecules, bound and unbound Copolymer 1 samples are separated on reverse phase HPLC using an acetonitrile gradient. Control, untreated Copolymer 1 elutes as a very broad peak with several smaller peaks, which spread between approximately 40 and 75 min elution time. This elution profile is characteristic of a mixture of random polypeptides and resembles HPLC separations of other batches of Copolymer 1. Similar profiles were obtained when Copolymer 1 was eluted from HLA-DR1, HLA-DR2 or HLA-DR4 molecules, indicating that the bound fraction is similar to the original Copolymer 1 preparation in its chemical properties.

At least 95 % of the added Copolymer 1 molecules are observed in the fraction bound to isolated HLA-DR1 proteins; similarly, at least 95 % of the added

Copolymer 1 molecules are observed in the fraction bound to isolated HLA-DR4 proteins. However, 80% of the added Copolymer 1 molecules are bound to HLA-DR2 proteins. Copolymer 1 eluted from the HLA complexes with had a ratio of amino acids tyrosine: glutamic acid: alanine: lysine which was similar to that of control untreated Copolymer 1. These results indicate that the bound fraction of Copolymer 1 had an amino acid composition like that of the bound/unbound mixture and that the population of Copolymer 1 molecules exhibited little or no preferential binding to different HLA-DR proteins.

To analyze the sequence of Copolymer 1 that bound to each of HLA-DR1, -DR2 and -DR4 molecules, HPLC fractions obtained above were pooled submitted to automated Edman degradation on a Hewlett-Packard G1005A (Palo Alto, CA) protein sequencer using the manufacturer's Routine 3.5.

For each HLA-DR protein, the bound copolymer had a random distribution of the four amino acid which corresponded to the input molar ratios of amino acids used for making Copolymer 1. Alanine was found at significantly higher levels compared to glutamic acid, tyrosine and lysine, as is expected from the initially higher molar ratio of alanine in Copolymer 1. No sequence specificity or preferential positioning of any of the amino acids of Copolymer 1 was observed, indicating that the bound fraction was also random and similar to the unfractionated Copolymer 1 preparation.

Characterization of Bound and Unbound Copolymer 1 Epitopes

Anti-Copolymer 1 polyclonal antibodies were used to determine whether the Copolymer 1 fractions eluted from each of the HLA-DR molecules contained the epitopes found in control untreated Copolymer 1. Cross reactivity between Copolymer 1 and various eluted fractions was detected by direct ELISA assay using biotinylated anti-Copolymer 1 polyclonal antibodies. Copolymer 1 or Copolymer 1 fractions were diluted to 0.4 $\mu\text{g/ml}$ and 2.0 $\mu\text{g/ml}$ and 100 $\mu\text{g/well}$ was plated in duplicate on a 96-well microtiter immunoassay plate (PRO-BIND™, Falcon, Lincoln Park, NJ), incubated for 1 hr at 37°C and washed three times with TBS containing

0.05% Tween-20. The wells were then blocked with TBS containing 3% BSA, followed by addition of biotinylated anti-Copolymer 1 antibodies (at a dilution of 1:5000, 100 μ l/well). Antibody-ligand complexes were detected using streptavidin-conjugated alkaline phosphatase (at a dilution of 1:3000, BioRad) and *p*-nitrophenyl phosphate in triethanolamine buffer (BioRad; Hercules, CA). The absorption at 410 nm was monitored by a microplate reader (Dynatech MR4000).

The antibody binding assays showed that all the fractions were similarly recognized by anti-copolymer antibodies, suggesting that these bound heteropolymer fractions shared similar or identical epitopes with each other and with control Copolymer 1.

Characterization of Copolymer 1-HLA binding motifs

When bound, the MHC class II protein protects the Copolymer 1 binding site from peptidase digestion. To obtain the amino acid sequence(s) of the binding site(s) within Copolymer 1 for HLA-DR molecules, 1 mM Copolymer 1 was separately incubated with 100 μ M of each type of HLA-DR molecule in a volume of 10 μ l PBS for 40 hours at 37°C, so that the molar ratio of Copolymer 1 to HLA-DR was 10:1. Two units of aminopeptidase I was added to the reaction for the last 18 hr of incubation. Aminopeptidase I is a metalloprotein isolated from *Streptomyces griseus* (Spungin et al. 283 J. BIOCHEM. 471 (1989)) and is available from Sigma Chemicals, St. Louis, MO. Aminopeptidase I removes the amino-terminal ends of Copolymer 1 which protrude from the HLA-DR molecules, and digests the remaining unbound Copolymer 1 (Mouritsen et al. 148 J. IMMUNOL. 1987 (1992); Larsen et al. 184 J. EXP. MED. 183 (1996)). Subsequent digestions of Copolymer 1 with aminopeptidase are performed in volumes scaled up by a factor of twenty-four fold, for example, 300 μ l of heteropolymer digested with 60 μ l of aminopeptidase. Samples are spin-concentrated to a final volume of approximately 100 μ l using Centricon 10 ultrafiltration devices.

The Copolymer 1-HLA-DR complexes and the unbound Copolymer 1 were analyzed by SDS-PAGE, using a NOVEX mini-cell electrophoresis system, a 10%

acrylamide separating gel and a 5% acrylamide stacking gel. The Copolymer 1-HLA-DR1 complexes were run under non-reducing conditions for 1 hr at 200 V, stained with Coomassie Brilliant Blue, fixed for 3 hr in 10% methanol/10% acetic acid and dried on Cellophane paper (BioRad) at 25°C. The Copolymer 1-HLA-DR complexes were found to be resistant to SDS-mediated dissociation, forming higher molecular weight complexes with HLA-DR1 $\alpha\beta$ heterodimers, and were observed as numerous bands on the polyacrylamide gel with molecular weights greater than 50 kD, indicating that the Copolymer 1-HLA-DR complexes were protected. Aminopeptidase I treatment resulted in unbound Copolymer 1 appearing as a smear in the lower part of the gel, indicating that it was completely digested by the enzyme.

Fractions containing the peaks of Copolymer 1-HLA-DR complexes were selected in the region between approximately 40 and 75 min elution time for each class of HLA-DR complex to obtain the sequence of the binding motifs. Bound, digested Copolymer 1 polypeptides, which lack the protruding N-termini, are eluted from HLA-DR by addition of acetic acid (10%) and incubation at 70°C for 15 min, followed by ultrafiltration and vacuum concentration in a SpeedVac (Savant Instruments, Farmingdale, NY). Fridkis-Hareli et al. 163 CELL. IMMUNOL. 229 (1995).

The N-terminal 20 to 25 amino acids of Copolymer 1 protrude beyond the HLA-DR proteins, and are not part of the binding motifs of Copolymer 1 for these proteins. The sequence data (Table 9) show that Copolymer 1 peptides bound to HLA-DR1 have significantly higher levels of glutamine at the first and second positions of the Copolymer 1 binding domain, higher levels of lysine at the second and third positions, and higher levels of tyrosine at the third to fifth positions. The third position of the bound Copolymer 1 peptide (lysine or tyrosine) may correspond to the P1 position of the peptide binding site within the MHC class II groove because the P1 site is the third amino acid in the binding sites of other peptides which bind HLA-DR1. For example, tyrosine is found in the third (P1) position of the HA 306-318 peptide, which corresponds to the Y308 position of the HA protein. Stern et al., 368 NATURE (Lond.) 215. These data are in contrast to the random patterns of the sequences found in untreated Copolymer 1, which shows no sequence specificity or

preferential positioning within the MHC class II groove for any of the four amino acids within Copolymer 1.

For HLA-DR2, both tyrosine and alanine are detected after the third cycle of Edman degradation (Table 9). No sequence specificity or preferential positioning is observed for positions corresponding to anchor positions following P1 (at positions corresponding to the P4, P6 or P9 positions of HLA-DR1 and HLA-DR4; and at positions corresponding to the P4 or P7 positions of HLA-DR2b molecules). In all the samples the levels of alanine are higher than those of glutamine, tyrosine and lysine, which was expected because a higher molar ratio of alanine is present in Copolymer 1. For each of the HLA-DR1 and HLA-DR4 molecules, tyrosine was found at the position corresponding to the first anchor position (the third residue in the sequence analysis), followed by alanine in the positions corresponding to the subsequent pockets. In the Copolymer 1 bound to HLA-DR-2, tyrosine was also enriched at the position corresponding to P1. Glutamic acid was enriched at the first cycle position corresponding to the P-2 position and at the next adjacent position corresponding to P-1, lysine was enriched. These residues can contribute to the stable interactions of Copolymer 1 with the HLA-DR molecules and the interaction of this complex with the T cell receptor (TCR).

These results indicate that Copolymer 1 contains class II MHC binding motifs. It may be that Copolymer 1 bound to the antigen groove of HLA-DR molecules can act either as a blocking peptide or as an antagonist or partial agonist, resulting in suppression of autoimmune T cell responses or anergy, or both. Applicants' invention does not depend upon the theory underlying the action of Copolymer 1 or terpolymers.

Table 9

**Binding sequences of Copolymer 1 Peptides
Bound to HLA-DR1, HLA-DR2 and HLA-DR4 molecules**

HLA-DR	relative amino acid positions						
	-2	-1	1	4	6	7	9
DRBI*0101 DR-1	E	K	Y	A	A	A	A
DRBI*0401 DR-4	E	K	Y	A	A	A	A
DRBI*1501 DR-2	E	K	Y,A	A	A	A	A

EXAMPLE 11**DEVELOPMENT OF PEPTIDES FOR BINDING****HLA-DR1 AND HLA-DR4 MOLECULES**

The previous examples indicate that Copolymer 1 and Terpolymers bind to purified human HLA-DR molecules within the peptide binding groove and inhibit binding of HA 306-318, a peptide from influenza virus which binds with high affinity to both HLA-DR1 (DRB 1*0101) and HLA-DR4 (DRB 1*0401) molecules. Further, terpolymers composed of only three amino acids (GAL, TGA, TAL and GTL) bound to purified HLA-DR1, HLA-DR2 and HLA-DR4 molecules and competed with the collagen peptide, CII 261-273, for binding to RA-associated HLA-DR1 (DR-B I *0101) and -DR4 (DRB 1*0401) protein molecules. The terpolymers also inhibited CII-reactive T cell clones.

In this example, peptides of defined sequence and length (15 residues) were synthesized using the sequences of the binding motifs summarized in Table 9. These peptides were analyzed for affinity and specificity of binding to MHC class II HLA-DR protein molecules, for an ability to inhibit binding of competitor molecules and for an ability to inhibit T cell responses. According to the present invention, these properties are useful in therapeutic compositions for treating immune diseases.

Peptides shown in Table 10 were synthesized using solid phase techniques (Barany, G. et al., 1979. *The Peptides*, E. Gross et al., eds. (New York, NY:

Academic Press) on an Applied Biosystems Peptide Synthesizer, and were purified by reversed-phase HPLC. Peptide sequences included HA 306-318, having the sequence PKYVKQNTLKLAT (SEQ ID NO: 2)(MW 1718); CII 261-273, having the sequence AGFKGEQGPKGEP (SEQ ID NO: 3)(MW 1516); and HA 306-318 bracketed by alanines at the N- and C-terminals, APKYVKQNTLKLATA (SEQ ID NO: 44). Peptides were also synthesized on a 1 μ mole scale using the Multipin Peptide Synthesis System (Chiron Technologies, Raleigh, NC). Peptides were synthesized as 15-mers with free amino groups at the N-terminus and free carboxyl groups at the C-terminus, and with biotin linked to the N-terminus by the spacer SGSG and having a free carboxyl group at the C-terminus. Peptide synthesis was monitored by including two standard peptide sequences as controls, which were subjected to HPLC and mass spectroscopy analysis. The HA 306-318 peptide was also used as a positive control for binding experiments. Pin peptides were lyophilized and resuspended at a concentration of 2 mg/ml in dimethyl sulfoxide (DMSO). Under these conditions, the majority of peptides were completely solubilized. Biotinylation was performed with excess N-hydroxysuccinimide biotin (Sigma, St. Louis, MO) in DMSO as described in Fridkis-Hareli et al., 91 PROC. NAD. ACAD. SCI., USA 4872-4876 (1994). Unreacted biotin was removed by dialysis (SpectraPor® membrane MWCO 500, Spectrum Medical Industries, Houston, TX).

Peptides were made to have test sequence motifs for binding to the groove of HLA-DR1 and -DR4 molecules (see Table 10). The peptides generally contained various combinations of glutamic acid, lysine and alanine at the N-terminus, followed by tyrosine at the position corresponding to P1 (shown in bold in Table 10), and then alanine in the subsequent binding pockets. The test sequence motifs fall into three different groups according to these positions in the consensus (Table 10). Peptides in group I had lysine (K) at the position corresponding to P8 and tyrosine (Y) at the position corresponding to P1 (in bold in Table 10). A reference peptide in this set with lysine (K) at the position corresponding to P8 to increase solubility and alanine at all other residues (SEQ ID NO: 45) has previously been synthesized. Jardetzky et al., 9 EMBO J. 1797-1803 (1990). Peptides in group II had tyrosine (Y) at the

position corresponding to P1, but had alanine (A) at the position corresponding to P8. Peptides in group III had amino acid tyrosine (Y) shifted one or two residues with respect to the P1 position in HA 306-318 peptide. Peptides in all groups contained one or more glutamic acid (E) and/or lysine (K) residues, in variable positions as was observed in the binding motifs supra, and to enhance solubility. Both N-terminal biotinylated and unlabeled sets of peptides were synthesized for these studies.

Table 10
Groups of synthetic peptides and consensus positions

Group	SEQ ID NO	peptide sequence	amino acid consensus positions
Control	44	APKYVKQNTLKLATA	A(HA 306-318)A
I	45	AAAYAAAAAAKAAAA	P1Y, P8K
	46	AKKYAAAAAAKAAAA	
	47	AEAYAAAAAAKAAAA	
	25	AKEYAAAAAAKAAAA	
	26	AAEYAAAAAAKAAAA	
	27	AAKYAEAAAAKAAAA	
	28	EAKYAAAAAAKAAAA	
	29	AEKYAAAAAAKAAAA	
	30	KEAYAAAAAAKAAAA	
	31	AEKYAAAAAAKAAAA	
	32	EKAYAAAAAAKAAAA	
	33	AAKYEA AAAAKAAAA	
	34	EAAYAAAAAAKAAAA	
	35	EKKYAAAAAAKAAAA	
II	48	AEKYAAAAAAAAAAAA	P1Y, P8A
	49	AKEYAAAAAAAAAAAA	
	50	AKKYAEAAAAAAAAAAAA	
	51	AEAYKAAAAAAAAAAAA	
	52	KEAYAAAAAAAAAAAA	
	53	AEKYAAAAAAAAAAAA	
	54	EKAYAAAAAAAAAAAA	
	55	EKKYAAAAAAAAAAAA	
	56	EAKYAAAAAAAAAAAA	
	36	AKKYEA AAAAKAAAA	
	37	AAEYKAAAAAAAAAAAA	
	38	AAKYEA AAAAKAAAA	
	39	AAKYAEAAAAAAAAAAAA	
III	40	AEYAKAAAAAAAAAAAA	P1A, P8A
	41	AEKAYAAAAAAAAAAAA	
	57	EKYAAAAAAAAAAAAA	
	42	AYKAEAAAAAAAAAAAA	
	43	AKYAEAAAAAAAAAAAA	

Competitive binding assays are used to examine whether the synthetic peptides can compete successfully with Copolymer 1 or with the high affinity HA 306-318 peptide for binding to HLA-DR1 and HLA-DR4 proteins. In the competitive binding assays, either Copolymer 1 or the HA 306-318 peptide bracketed by alanines (APKYVKQNTLKLATA, SEQ ID NO: 44) is biotinylated and unlabeled Copolymer 1 or peptide inhibitors are added. Kinetic studies indicated that biotinylated Copolymer 1 inhibited binding of unlabeled Copolymer 1 and of HA 306-318 (SEQ ID NO: 2) to recombinant HLA-DR1 better than peptides of groups I-III. However, several peptides containing lysine at the P8 position (group I) are better inhibitors than peptides of similar sequence but with an alanine at the P8 position (groups II and III of Table 10). In contrast, the binding of biotinylated Copolymer 1 to HLA-DR4 molecules was efficiently inhibited by many of the peptides in groups I-III. Conversely, the binding of biotinylated HA 306-318 to HLA-DR4 was inhibited more by Copolymer 1 than by HA 306-318 or by the peptides of groups I-III.

To further characterize the relative affinity of the Group I-III peptides for binding to HLA-DR1, -DR2 and -DR4 molecules, competitive binding assays are performed with biotinylated Multipin peptides using unlabeled Copolymer 1, HA 306-318 or CII 261-273 as inhibitors. The binding of the majority of Group I-III peptides to HLA-DR1 and HLA-DR4 was inhibited by unlabeled Copolymer 1, HA 306-318 (SEQ ID NO: 2) and CII 261-273 (SEQ ID NO: 3), however, less efficiently than the binding of HA 306-318 (SEQ ID NO: 2). Some of the peptides showed higher affinity for the HLA-DR1 (Table 11A) or HLA-DR4 (Table 11B) proteins than did Copolymer 1, HA 306-318, or CII 261-273.

Table 11A
Affinity of Group I-III peptides for HLA-DR1 molecules

SEQ ID NO	peptide sequence	HA 306-318	Inhibitors Copolymer 1
44	APKYVKQNTLKLATA	13.0	3.3
25	AKEYAAAAAAKAAAA	19.0	
26	AAEYAAAAAAKAAAA	47.0	
27	AAKYAEAAAAKAAAA	42.0	16.0
28	EAKYAAAAAAKAAAA	33.0	
	Copolymer 1	10.0	8.0

Table 11B
Affinity of Selected Copeptides for HLA-DR4 (DRB1*0401)

Group	SEQ ID NO	peptide sequence	HA 306-318 (μ M)	Copolymer 1 (μ M)
Control	44	APKYVKQNTLKLATA	26.0	8.2
I	45	AAAYAAAAAAKAAAA	7.0	
	25	AKEYAAAAAAKAAAA	4.5	
	26	AAEYAAAAAAKAAAA	3.2	1.6
	27	AAKYAEAAAAKAAAA	1.8	<1.0
	28	EAKYAAAAAAKAAAA	4.4	3.0
	29	AEKYAAAAAAKAAAA	6.5	
	30	KEAYAAAAAAKAAAA	4.5	
	31	AEYAAAAAAKAAAA	2.0	
	32	EKAYAAAAAAKAAAA	3.3	
	33	AAKYEAAAAAAKAAAA	4.0	
	34	EAAYAAAAAAKAAAA	5.0	
	35	EKKYAAAAAAKAAAA	1.8	
	36	AKKYEAAAAA	2.2	
	37	AAEYKAAAAA	1.8	
	38	AAKYEAAAAA	1.2	
II	39	AAKYAEAAAAA	1.2	
	40	AEYAKAAAAA	3.0	
	41	AEKAYAAAAA	<1.0	
	42	AYKAEAAAAA	1.3	
	43	AKYAEAAAAA	3.0	
III				
		Copolymer 1	2.5	20.0

Affinities were determined by competition with biotinylated competitors HA306-318 and Copolymer 1.

All peptides were further tested for inhibition of CII-specific T cell responses

using methods described in previous examples. HA 306-318 (peptide SEQ ID NO: 2) inhibited both DR1 3.19 and 19.3 T cell clones very efficiently (over 95% and 98% for 19.3 and 3.19 cells, respectively). However, peptides with SEQ ID NO: 27, 48, 36 and 53 were as good or better inhibitors of T cell response than the reference influenza virus hemagglutinin peptide HA 306-318.

For HLA-DR4-restricted T cells, using L fibroblasts transfected with HLA-DR4 as the antigen presenting cell, the following pattern of activity was obtained: peptides SEQ ID NOS: 29, 31, 34, 35, 50, 51, 54, 38 and 41 were good inhibitors of the DR4 3838 T cell clone, whereas the D3 clone was inhibited best by peptides SEQ ID NOS: 46, 27, 34, 28 and 54. These peptides produced levels of inhibition of over 80% for the D3 and 3838 cells. Copolymer 1 had only a minimal effect on the CII-specific T cell response, consistently giving less than 20% inhibition. HA 306-318 (SEQ ID NO: 2) inhibited both DR4 3838 and D3 T cell clones less efficiently (less than 60% inhibition) than it inhibited the DR1, 3.19 and 19.3 clones.

These data show that peptides of SEQ ID NO: 46, 27, 34, 28 and 41 are significantly better inhibitors of T cell response than the reference influenza virus hemagglutinin peptide HA 306-318. Peptides of SEQ ID NO: 27 and 41 are high level inhibitors both of HLA-DR-1- and -DR-4-restricted CII-specific T cells.

The data in these examples, performed with each peptide at least in duplicate, show that of 33 unique synthetic peptides, several inhibited binding of HA 306-318 and Copolymer 1 to recombinant HLA-DR1 and -DR4 molecules. Peptides which inhibited binding of HA 306-318 or copolymer1 to HLA-DR1 or -DR4 molecules contained tyrosine at the PI position. The presence of glutamic acid, alanine and lysine in various combinations on the N-terminal side of PI did not seem to influence the affinity of the binding. Of the subsequent residues, lysine at P8 was important for inhibition of HA 306-318 but not of Copolymer 1 binding to HLA-DR1. In contrast to HLA-DR1, a larger number of peptides inhibited binding of both HA 306-318 and Copolymer 1 to HLA-DR4 molecules. These peptides contained tyrosine at the position corresponding to P1 and either lysine or alanine at the position corresponding to P8, with no apparent preference for specific amino acids at

other positions.

The affinity of the HA 306-318 for recombinant HLA-DR4 was lower, and that of Copolymer 1 higher, than for HLA-DR1 molecules. These affinities are similar to those observed with HLA-DR1 and -DR4 molecules purified from human blood. The binding of some of the biotinylated peptides to either HLA-DR1 or -DR4 was inhibited by CII 261-273, as well as by HA 306-318 and Copolymer 1, showing that these peptides may compete for presentation to CII-reactive T cells, in a similar fashion to that for the whole Copolymer 1 mixture. Peptides with an affinity close to or higher than that of CII 261-273, HA 306-318 and Copolymer 1 preparations are listed in Table 11A, for HLA-DR1 and Table 11B, for HLA-DR4.

Several of the 15-mer peptides inhibited type II collagen-specific T cell clones. These peptides all had tyrosine at the position corresponding to P1 and either lysine or alanine at the position corresponding to P8, with no other specific sequence patterns. The examples provided here show the strong inhibition by several random heteropolymers composed of three amino acids selected from the group consisting of tyrosine, glutamic acid, alanine and lysine. These heteropolymers, especially TAL, competed with CII 261-273 for binding to RA-associated HLA-DR1 and -DR4 molecules, and inhibited CII-reactive T cell clones. Further, peptide SEQ ID NO: 46, which includes the direct sequence tyrosine-alanine-lysine inhibited type II collagen-reactive T cells better than Copolymer 1, indicating that a peptide of approximately 15 amino acids in length having single tyrosine-alanine-lysine sequence can substitute for the mixture of random polypeptides found in the TAL heteropolymer.

The results of the foregoing examples indicate that the embodiments of the invention, with individual amino acid sequences that include at least three amino acids selected from tyrosine, glutamic acid, alanine and lysine, have binding motifs for anchor positions fitting particular HLA-DR molecules and can act as effective therapeutic agents for autoimmune diseases. A pharmaceutical composition comprising a pure synthetic short polypeptide of single sequence may have fewer side effects and greater specificity for a particular binding site or autoimmune

disease than a mixture of polypeptides of random sequence. On the other hand, the polypeptide mixtures contemplated by the present invention may have broader efficacy for many types of autoimmune diseases. Hence, both the short polypeptides of a single sequence, and the mixtures of polypeptides easily provided by the present invention, are valuable therapeutic agents.

EXAMPLE 12

COPOLYMER 1 INHIBITS ACTIVATION OF T CELLS RESPONSIVE TO A MYASTHENIA GRAVIS ANTIGENIC PEPTIDE

METHODS

Copolymer 1

Copolymer 1 was obtained from Teva Pharmaceutical Industries (Petach Tikva, Israel).

Myasthenia Gravis-Related Peptides were synthesized on an Applied Biosystems Peptide Synthesizer using solid phase techniques. Barany et al., *THE PEPTIDES* 1 (1979). Peptides were purified by reversed-phase HPLC. The peptides used were the p259 peptide, see Zisman et al., *Hum Immunol* 1995 Nov; **44**(3):121-30; Brocke et al., *Immunology* 1990 Apr; **69**(4):495-500

IL-2 secretion

Secretion of IL-2 by the cell line WCB AB. in response to the myasthenia gravis peptides and/or Copolymer 1 were evaluated. Cells (1.5×10^4) were incubated with the indicated antigen. Secretion of IL-2 by the cell line WCB AB was used as a measure of activation of that T-cell line.

RESULTS

Table 12 indicates that the p259 peptide stimulates T cell secretion. However, when Copolymer 1 is incubated with the p259 peptide, T cell secretion of IL-2 is inhibited in a dose-related fashion. At 100 μ M Copolymer 1 inhibits about

91% of IL-2 secretion (Table 13), indicating that Copolymer 1 is a potent inhibitor of T cell activation.

Table 12
IL-2 secretion from WCB AB line in response to p259

p 259 conc. (μ M)	Avg OD (450 nm)	SD	%CV	IL-2 (pg/ml)
0	0.077	0.01		0
0.25	0.135	0.00		24
0.5	0.227	0.01	3.9	72
1	0.387	0.01	2.9	159
2	0.725	0.02	2.4	347

Table 13
IL-2 secretion from WCB AB line
in response to Cop1 alone or 2 μ M p259 + Cop1

Cop1 (μ M)	Avg OD (450 nm)	SD	%CV	IL-2 (pg/ml)	% Inhibition
0	0.725	0.02	2.4	347	
1	0.086	0.01		0	
2	0.079	0.00		0	
10	0.086	0.00		0	
20	0.266	0.01	8.0	93	73
60	0.166	0.01		40	88
100	0.151	0.01	11.2	32	91

Absorbance is the average of 3 samples. Confidence values were calculated relative to the absorbance of a blank (%CV = SD/(Avg-blank)*100).

WHAT IS CLAIMED:

1. A terpolymer consisting essentially of tyrosine, alanine and lysine randomly polymerized into a polypeptide.
2. The terpolymer of Claim 1 which is substantially free of glutamic acid.
3. The terpolymer of Claim 1 wherein said tyrosine is present in a mole fraction of about 0.005 to about 0.250; said alanine is present in a mole fraction of about 0.3 to about 0.6; and lysine is present in a mole fraction of about 0.1 to about 0.5.
4. The terpolymer of Claim 1 wherein said tyrosine is present in a mole fraction of about 0.10, said alanine is present in a mole fraction of about 0.54, and said lysine is present in a mole fraction of about 0.35.
5. A terpolymer consisting essentially of glutamic acid, tyrosine and lysine randomly polymerized into a polypeptide.
6. The terpolymer of Claim 5 which is substantially free of alanine.
7. The terpolymer of Claim 5 wherein said glutamic acid is present in a mole fraction of about 0.005 to about 0.300; said tyrosine is present in a mole fraction of about 0.005 to about 0.250; and said lysine is present in a mole fraction of about 0.3 to about 0.7.
8. The terpolymer of Claim 5 wherein said glutamic acid is present in a mole fraction of about 0.26, said tyrosine is present in a mole fraction of about 0.16 and said lysine is present in a mole fraction of about 0.58.
9. A terpolymer consisting essentially of glutamic acid, alanine and lysine

randomly polymerized into a polypeptide.

10. The terpolymer of Claim 9 which is substantially free of tyrosine.
11. The terpolymer of Claim 9, wherein said glutamic acid is present in a mole fraction of about 0.005 to about 0.300; said alanine is present in a mole fraction of about 0.005 to about 0.600; and said lysine is present in a mole fraction of about 0.2 to about 0.7.
12. The terpolymer of Claim 9 wherein said glutamic acid is present in a mole fraction of about 0.15, said alanine is present in a mole fraction of about 0.48 and said lysine is present in a mole fraction of about 0.36.
13. A terpolymer consisting essentially of tyrosine, glutamic acid and alanine randomly polymerized into a polypeptide, wherein said tyrosine is present in a mole fraction of about 0.005 to about 0.250; said glutamic acid is present in a mole fraction of about 0.005 to about 0.300, and said alanine is present in a mole fraction of about 0.005 to about 0.800.
14. The terpolymer of Claim 13 wherein said tyrosine is present in a mole fraction of about 0.14, said glutamic acid is present in a mole fraction of about 0.21, and said alanine is present in a mole fraction of about 0.65.
15. The terpolymer of Claim 13 which is substantially free of tyrosine.
16. A pharmaceutical composition for the treatment of an autoimmune disease, comprising a therapeutically effective amount of a terpolymer comprising three different amino acids randomly polymerized into a polypeptide, and a pharmaceutically acceptable carrier, wherein said three different amino acids are selected from the group of tyrosine, glutamic acid, alanine and lysine.

17. The pharmaceutical composition of Claim 16 wherein said terpolymer consists essentially of tyrosine, alanine and lysine.
18. The pharmaceutical composition of Claim 17 wherein said terpolymer is substantially free of glutamic acid.
19. The pharmaceutical composition of Claim 17 wherein said tyrosine is present in a mole fraction of about 0.005 to about 0.250; said alanine is present in a mole fraction of about 0.3 to about 0.6; and lysine is present in a mole fraction of about 0.1 to about 0.5.
20. The pharmaceutical composition of Claim 17 wherein said tyrosine is present in a mole fraction of about 0.10, said alanine is present in a mole fraction of about 0.54, and said lysine is present in a mole fraction of about 0.35.
21. The pharmaceutical composition of Claim 16 wherein said terpolymer consists essentially of glutamic acid, tyrosine and lysine.
22. The pharmaceutical composition of Claim 21 wherein said polypeptide is substantially free of alanine.
23. The pharmaceutical composition of Claim 21 wherein said glutamic acid is present in a mole fraction of about 0.005 to about 0.300; said tyrosine is present in a mole fraction of about 0.005 to about 0.250; and said lysine is present in a mole fraction of about 0.3 to about 0.7.
24. The pharmaceutical composition of Claim 21 wherein said glutamic acid is present in a mole fraction of about 0.26, said tyrosine is present in a mole fraction of about 0.16 and said lysine is present in a mole fraction of about

0.58.

25. The pharmaceutical composition of Claim 16 wherein said terpolymer consists essentially of glutamic acid, alanine and lysine.
26. The pharmaceutical composition of Claim 25 wherein said polypeptide is substantially free of tyrosine.
27. The pharmaceutical composition of Claim 25, wherein said glutamic acid is present in a mole fraction of about 0.005 to about 0.300; said alanine is present in a mole fraction of about 0.005 to about 0.600; and said lysine is present in a mole fraction of about 0.2 to about 0.7.
28. The pharmaceutical composition of Claim 25 wherein said glutamic acid is present in a mole fraction of about 0.15, said alanine is present in a mole fraction of about 0.48 and said lysine is present in a mole fraction of about 0.36.
29. The pharmaceutical composition of Claim 16 wherein said terpolymer consists essentially of tyrosine, glutamic acid and alanine, and wherein said tyrosine is present in a mole fraction of about 0.005 to about 0.250; said glutamic acid is present in a mole fraction of about 0.005 to about 0.300, and said alanine is present in a mole fraction of about 0.005 to about 0.800.
30. The pharmaceutical composition of Claim 29 wherein said tyrosine is present in a mole fraction of about 0.14, said glutamic acid is present in a mole fraction of about 0.21, and said alanine is present in a mole fraction of about 0.65.
31. The pharmaceutical composition of Claim 29 which is substantially free of

lysine.

32. The pharmaceutical composition of Claim 16 wherein said terpolymer has a molecular weight of about 2,000 to about 40,000 daltons.
33. The pharmaceutical composition of Claim 16 wherein said terpolymer has a molecular weight of about 4,000 to about 9,000 daltons.
34. The pharmaceutical composition of Claim 16, wherein said autoimmune disease is a B cell mediated autoimmune disease.
35. The pharmaceutical composition of Claim 16, wherein said autoimmune disease is a T cell mediated autoimmune disease.
36. The pharmaceutical composition of Claim 16, wherein said autoimmune disease is an arthritic condition.
37. The pharmaceutical composition of Claim 16, wherein said autoimmune disease is a demyelinating disease.
38. The pharmaceutical composition of Claim 16, wherein said autoimmune disease is an inflammatory disease.
39. The pharmaceutical composition of Claim 16, wherein said autoimmune disease is multiple sclerosis, autoimmune hemolytic anemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, chronic immune thrombocytopenic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis, or systemic lupus erythematosus.

40. A method for treating an autoimmune disease in a mammal which comprises administering a therapeutically effective amount of a terpolymer polypeptide comprising three different amino acids randomly polymerized into a polypeptide, wherein said three different amino acids are selected from the group of tyrosine, glutamic acid, alanine and lysine.
41. The method of Claim 40 wherein said terpolymer polypeptide consists essentially of tyrosine, alanine and lysine.
42. The method of Claim 40 wherein said terpolymer polypeptide consists essentially of glutamic acid, tyrosine and lysine.
43. The method of Claim 40 wherein said terpolymer polypeptide consists essentially of glutamic acid, alanine and lysine.
44. The method of Claim 40 wherein said terpolymer polypeptide consists essentially of tyrosine, glutamic acid and alanine, and wherein said tyrosine is present in a mole fraction of about 0.005 to about 0.250; said glutamic acid is present in a mole fraction of about 0.005 to about 0.300, and said alanine is present in a mole fraction of about 0.005 to about 0.800.
45. A method for treating an autoimmune disease which comprises administering a therapeutically effective amount of a polypeptide consisting essentially of amino acids tyrosine, glutamic acid, alanine and lysine, wherein said autoimmune disease is not multiple sclerosis.
46. The method of Claim 40 or 45, wherein said polypeptide inhibits activation of T cells.

47. The method of Claim 40 or 45, wherein said polypeptide activates T cell suppressor mechanisms.
48. The method of Claim 40, wherein said polypeptide inhibits activation of T cells responsive to myelin basic protein.
49. The method of Claim 40 or 45, wherein said polypeptide inhibits activation of T cells responsive to collagen type II peptide.
50. The method of Claim 40 or 45, wherein said polypeptide binds to a class II MHC protein.
51. The method of Claim 40 or 45, wherein said polypeptide binds to HLA-DR1.
52. The method of Claim 40 or 45, wherein said polypeptide binds to HLA-DR2.
53. The method of Claim 40 or 45, wherein said polypeptide binds to HLA-DR4.
54. The method of Claim 40 or 45, wherein said polypeptide binds to an antigen presenting cell.
55. The method of Claim 40, wherein said autoimmune disease is multiple sclerosis.
56. The method of Claim 40 or 45, wherein said autoimmune disease is autoimmune hemolytic anemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, chronic immune thrombocytopenic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis, or

systemic lupus erythematosus.

57. The method of Claim 40 or 45, wherein said polypeptide has a molecular weight of about 2,000 to about 40,000 daltons.
58. The method of Claim 40 or 45, wherein said polypeptide has a molecular weight of from about 4,000 to about 12,000 daltons.
59. A synthetic peptide having an amino acid sequence comprising at least three amino acids selected from the group of amino acids consisting of aromatic amino acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids, wherein the synthetic peptide is at least seven amino acid residues in length and is capable of binding to an MHC class II protein associated with an autoimmune disease.
60. The synthetic peptide of Claim 59 in which the aromatic amino acid is selected from the group consisting of tyrosine, valine, and phenylalanine.
61. The synthetic peptide of Claim 59, in which the positively charged amino acid is lysine, and the sequence comprises
lysine-tyrosine; lysine-valine; or lysine-phenylalanine.
62. The synthetic peptide of Claim 59, wherein the negatively charged amino acid is glutamic acid, and the sequence comprises
glutamic acid-lysine-tyrosine;
glutamic acid-lysine-valine; or
glutamic acid-lysine-phenylalanine.
63. The synthetic peptide of Claim 59, wherein the aliphatic amino acid is alanine, and the sequence comprises

glutamic acid -lysine-tyrosine-alanine;
glutamic acid-lysine-valine-alanine; or
glutamic acid-lysine-phenylalanine-alanine.

64. The synthetic peptide of Claim 59, wherein the sequence comprises an amino-terminal alanine, and
alanine-glutamic acid-lysine-tyrosine-alanine;
alanine-glutamic acid-lysine-valine-alanine; or
alanine-glutamic acid-lysine-phenylalanine-alanine.
65. The synthetic peptide of Claim 59, wherein the aliphatic amino acid is alanine and the sequence comprises
lysine-glutamic acid-tyrosine-alanine;
lysine-tyrosine-alanine-glutamic acid;
lysine-glutamic acid-valine-alanine;
lysine-valine-alanine-glutamic acid;
lysine-glutamic acid-phenylalanine-alanine; or
lysine-phenylalanine-alanine-glutamic acid.
66. The synthetic peptide of Claim 59, wherein the aliphatic amino acid is alanine and the sequence comprises
lysine-tyrosine-alanine-alanine;
lysine-lysine-tyrosine-alanine;
lysine-valine-alanine-alanine;
lysine-lysine-valine-alanine;
lysine-phenylalanine-alanine-alanine; or
lysine-lysine-phenylalanine-alanine.
67. The synthetic peptide of Claim 59, wherein the peptide further comprises two alanine residues and the sequence comprises

alanine-lysine-tyrosine-alanine-glutamic acid;
glutamic acid-alanine-lysine-tyrosine-alanine;
alanine-lysine-valine-alanine-glutamic acid;
glutamic acid-alanine-lysine-valine-alanine;
alanine-lysine-phenylalanine-alanine-glutamic acid; or
glutamic acid-alanine-lysine-phenylalanine-alanine.

68. The synthetic peptide of Claim 64, wherein the autoimmune disease is an arthritic condition.
69. The synthetic peptide of Claim 68, wherein the arthritic condition is rheumatoid arthritis.
70. A composition according to Claim 59 wherein the peptide is 7-100 amino acid residues in length.
71. A composition which is a synthetic peptide having therapeutic activity in a subject suffering from an autoimmune disease, the amino acid sequence of said peptide having at least one of each of amino acids glutamic acid, lysine, and alanine and an amino acid selected from the group consisting of tyrosine, valine, and phenylalanine.
72. A composition according to Claim 71 wherein the peptide is 7-100 amino acids in length.
73. A composition according to Claim 71 wherein the peptide is 7-50 amino acids in length.
74. A composition according to Claim 69 wherein the peptide is 7-25 amino acids in length.

75. A composition according to Claim 69 wherein the peptide is 7-15 amino acids in length.
76. A composition according to Claim 59 formulated as a unitary dosage in a pharmaceutically acceptable carrier.
77. A composition according to Claim 59 which is substantially pure.
78. A composition according to Claim 59 having greater affinity for the antigen binding groove of an MHC class II protein associated with the autoimmune disease than a type II collagen 261-273 peptide.
79. A composition according to Claim 71 comprising amino acid analogs at residue locations and in amounts sufficient to inhibit protease degradation of the peptide in the subject.
80. An isolated peptide composition having a sequence selected from the group consisting of: AKEYAAAAAAKAAAA (SEQ ID NO: 25), AA EYAAAAAAKAAAA (SEQ ID NO: 26), AAKYAEAAAAKAAAA (SEQ ID NO: 27), and EAKYAAAAAAKAAAA (SEQ ID NO: 28).
81. An isolated peptide according to any of the peptides of Claim 80 in which the tyrosine (Y) has been substituted by a valine (V) or a phenylalanine (F).
82. An isolated peptide composition having a sequence selected from the group consisting of: AEKYAAAAAAKAAAA (SEQ ID NO: 29), AKEYAAAAAAKAAAA (SEQ ID NO: 25), KEAYAAAAAAKAAAA (SEQ ID NO: 30), AEEYAAAAAAKAAAA (SEQ ID NO: 31), AA EYAAAAAAKAAAA (SEQ ID NO: 26), EKAYAAAAAAKAAAA (SEQ ID NO: 32), AAKYEAAAAAAKAAAA (SEQ ID

NO: 33), AAKYAEAAAAKAAAA (SEQ ID NO: 27), EAAYAAAAAAKAAAA (SEQ ID NO: 34), EKKYAAAAAAKAAAA (SEQ ID NO: 35), EAKYAAAAAAKAAAA (SEQ ID NO: 28), AKKYEAAAAAAAAAAAA (SEQ ID NO: 55), AA EYKAAAAAAAAAAAA (SEQ ID NO: 37), AAKYEAAAAAAAAAAAA (SEQ ID NO: 38), AAKYAEAAAAAAAAAAAA (SEQ ID NO: 39), AEYAKAAAAAAAAAAAA (SEQ ID NO: 40), AEKAYAAAAAAAAAAAA (SEQ ID NO: 41), AYKAEAAAAAAAAAAAA (SEQ ID NO: 42), and AKYAEAAAAAAAAAAAA (SEQ ID NO: 43), the peptide having high affinity for an MHC class II protein.

83. An isolated peptide according to any of the sequences of Claim 82 in which the tyrosine (Y) has been substituted by a valine (V) or a phenylalanine (F).
84. An isolated peptide composition having an amino acid sequence capable of inhibiting an immune response in a subject to an autoantigen, wherein a position in the amino acid sequence of the peptide that corresponds to an antigen binding pocket in a peptide binding groove of an MHC class II DR protein is identified as a particular amino acid.
85. An isolated peptide composition according to Claim 84 wherein the autoantigen is associated with a condition selected from the group consisting of multiple sclerosis and arthritis.
86. An isolated peptide composition according to Claim 84, wherein the MHC class II protein is selected from the group consisting of an MHC class II HLA-DR1 protein, and an MHC class II HLA-DR4 protein.
87. An isolated peptide composition according to Claim 84, wherein the MHC class II protein is an MHC class II HLA-DR2 protein.
88. An isolated peptide composition according to Claim 84, wherein the amino

acid residue in the position of the sequence that corresponds to the P1 pocket in the MHC class II peptide binding groove is selected from the group consisting of a tyrosine, a valine, and a phenylalanine.

89. An isolated peptide composition according to Claim 84, wherein the amino acid residue in a first amino acid position of the sequence that corresponds to the P1 pocket in the MHC class II peptide binding groove is alanine.
90. An isolated peptide composition according to Claim 84, wherein the amino acid residue located eight residues beyond the first amino acid position of the sequence that corresponds to the P1 pocket in the MHC class II peptide binding groove is selected from the group consisting of lysine and alanine.
91. A pharmaceutical preparation comprising a first peptide sequence and a second peptide sequence, wherein the preparation is a mixture of a first peptide and a second peptide of different amino acid sequences both according to Claim 84 in a pharmaceutically acceptable carrier, the first sequence having in addition a lysine residue and the second sequence having an alanine residue at the amino acid position eight residues beyond the amino acid corresponding to the P1 pocket in the MHC class II peptide binding groove.
92. A method of treating a subject having an autoimmune disease, comprising:
 - (a) selecting a therapeutic agent comprising a synthetic heteropolymer having at least two different amino acids, a first being an amino acid which is charged and a second being an amino acid which is hydrophobic, the amino acids being polymerized in a linear configuration, and a pharmaceutically acceptable carrier; and
 - (b) administering the therapeutic agent to the subject having the autoimmune disease;

with the proviso that when the autoimmune disease is multiple sclerosis the synthetic heteropolymer is other than Copolymer 1.

93. A method according to Claim 92, wherein in step (a) the charged amino acid is selected from the group consisting of lysine, glutamic acid, and aspartic acid.
94. A method according to Claim 92, comprising in step (a) having a third amino acid which is selected from the group of charged amino acids, the third amino acid being a different amino acid from the second amino acid.
95. A method according to Claim 92, wherein the hydrophobic amino acid is selected from the group consisting of valine, leucine, isoleucine, alanine, phenylalanine, and tyrosine.
96. A method according to Claim 95, wherein the heteropolymer comprises the amino acids lysine, alanine, and tyrosine.
97. A method according to Claim 95, wherein the heteropolymer comprises the amino acids lysine, glutamic acid, alanine, and phenylalanine.
98. A method according to Claim 95, wherein the heteropolymer comprises the amino acids lysine, glutamic acid, alanine, and valine.
99. A method according to Claim 96, wherein the heteropolymer of step (a) contains lysine, alanine, and tyrosine polymerized in a molar ratio of at least 3 moles of lysine per mole of tyrosine, and at least 4 moles of alanine per mole of tyrosine.
100. A method according to Claim 99, wherein the molar ratio of lysine : alanine :

tyrosine is 4.0 : 5.0 : 1.0.

101. A method according to Claim 95, wherein the heteropolymer of step (a) contains the amino acids glutamic acid : lysine : alanine polymerized in a molar ratio of 1.5 : 4.0 : 5.0.
102. A method according to Claim 93, wherein the heteropolymer contains the amino acids glutamic acid : alanine : tyrosine polymerized in a molar ratio of 1.5 : 5.0 : 1.0.
103. A method according to Claim 93, wherein the heteropolymer contains the amino acids glutamic acid : lysine : tyrosine polymerized in a molar ratio of 1.5 : 4.0 : 1.0.
104. A method according to Claim 92, wherein step (a) further comprises selecting the heteropolymer that inhibits binding of an antigenic peptide to an MHC class II protein.
105. A method according to Claim 92, wherein step (a) further comprises selecting the heteropolymer that inhibits class II-specific T cell responses to an MHC class II protein-peptide complex.
106. A method according to Claim 104, wherein the antigenic peptide is associated with an autoimmune disease.
107. A method according to Claim 105, wherein the MHC class II protein is associated with an autoimmune disease.
108. A method according to Claim 92, wherein step (b) further comprises supplementing the combined heteropolymer and carrier with at least an

additional therapeutic agent.

109. A method according to Claim 108, wherein step (b) further comprises selecting the additional therapeutic agent from the group consisting of an antibody, an enzyme inhibitor, an antibacterial agent, an antiviral agent, a steroid, a nonsteroidal anti-inflammatory agent, an antimetabolite, a cytokine, and a soluble cytokine receptor.
110. A method according to Claim 108, wherein step (b) further comprises selecting an additional therapeutic agent that is an inducer of synthesis of a cytokine in a subject.
111. A method according to Claim 109, wherein step (b) further comprises selecting a cytokine from the group consisting of interferon- β , interleukin-4 and interleukin-10.
112. A method according to Claim 109, wherein step (b) further comprises selecting an enzyme inhibitor from the group consisting of a protease inhibitor and a cyclooxygenase inhibitor.
113. A method according to Claim 108, wherein step (a) further comprises selecting the pharmaceutically acceptable carrier as suitable for administration to the subject by a route selected from the group consisting of intravenous, intramuscular, intraperitoneal, subcutaneous, oral, and transdermal administration.
114. A method of making a therapeutic heteropolymer composition, comprising:
 - (a) selecting three or more amino acids from the group consisting of charged amino acids, aliphatic amino acids, and aromatic amino acids;
 - (b) polymerizing the amino acids selected in step (a) into a heteropolymer

having a random linear configuration;

(c) obtaining the heteropolymer in step (b) that inhibits binding of an antigenic peptide to an MHC class II protein; and

(d) formulating in a pharmaceutically acceptable carrier, the heteropolymer that inhibits binding of an antigenic peptide to an MHC class II protein, to obtain a therapeutic heteropolymer composition.

115. A method according to Claim 114, wherein step (c) further comprises obtaining the heteropolymer that inhibits binding of an antigen which is an autoantigen to an MHC class II protein.
116. A method according to Claim 115, wherein the autoantigen in step (c) is collagen type II peptide 261-273 and the class II MHC protein is MHC HLA-DR1 or MHC HLA-DR4.
117. A method according to Claim 115, wherein the autoantigen in step (c) is myelin basic protein peptide 84-102 and the class II MHC protein is MHC HLA-DR2.
118. A method according to Claim 116, wherein step (c) further comprises obtaining the heteropolymer that, at a concentration of 1.5 micromolar, inhibits 50% binding of collagen type II peptide 261-273, at a concentration of at least 20 micromolar, to a class II MHC HLA-DR1 or MHC HLA-DR4 protein.
119. A method according to Claim 117, wherein step (c) further comprises obtaining the heteropolymer that, at a concentration of 1.5 micromolar, inhibits 50% binding of myelin basic protein peptide 84-102, at a concentration of at least 20 micromolar, to a class II MHC HLA-DR2 protein.
120. A method according to Claim 114, comprising prior to step (a) the additional

step of producing the class II MHC protein recombinantly in a non-mammalian cell.

121. A method for obtaining an MHC class II binding motif amino acid sequence in a mixture of synthetic peptide heteropolymers having therapeutic activity in a subject, comprising:
 - (a) binding the mixture of synthetic heteropolymers to MHC class II protein molecules to form heteropolymer-MHC protein complexes;
 - (b) removing by peptidase enzyme digestion the amino terminal amino acid residues of the heteropolymers protruding from the heteropolymer-MHC protein complex to align amino termini of the heteropolymers to the edge of the MHC protein complexes; and
 - (c) eluting the aligned heteropolymers from the MHC protein by dissociating the complexes to release the amino terminal aligned heteropolymers having the binding motif.
122. A method according to Claim 121 wherein an additional step (d) comprises determining the amino terminal sequence of the aligned heteropolymers, to identify the binding motif.
123. A method according to Claim 122 wherein an additional step (e) comprises comparing the amino terminal sequence of the aligned heteropolymers to the amino acid sequence of the synthetic heteropolymer composition.
124. A method according to Claim 121, wherein the MHC class II protein is associated with an autoimmune disease.
125. A method according to Claim 124, wherein the autoimmune disease is an arthritic condition or a demyelinating condition.

126. A method according to Claim 122, wherein an additional step (e) comprises synthesizing a plurality of peptide preparations, each peptide preparation having a binding motif amino acid sequence.
127. A method according to Claim 126 wherein an additional step (f) comprises determining the affinity of each of the synthesized peptides for the MHC class II protein.
128. A method for treating a subject having an arthritic condition, comprising:
 - obtaining a therapeutic composition which is a pure heteropolymer comprised of amino acids; and
 - administering the composition in an effective dosage to the subject, such that the arthritic condition is remediated.
129. A method according to Claim 128, wherein the effective dosage is at least 5 mg per day.
130. A method according to Claim 128, wherein the effective dosage is at least 10 mg per day.
131. A method according to Claim 128, wherein the effective dosage is at least 15 mg per day.
132. A method according to Claim 128, wherein the effective dosage is at least 20 mg per day.
133. A method according to Claim 128, wherein the effective dosage is substantially in the range of 25 to 400 μ g per kg of the subject per day.
134. A kit for assaying the binding of an analyte to an MHC protein, comprising a

water-soluble MHC protein which has been recombinantly produced in a non-mammalian cell, a reaction chamber for containing the analyte and the MHC protein, means for detecting binding of the analyte to the MHC protein, a container, and instructions for use.

135. A kit according to Claim 134, wherein the MHC protein is an MHC class II protein selected from the group consisting of an MHC class II HLA-DR1, an MHC class II HLA-DR2 and an MHC class II HLA-DR4 protein.
136. A kit according to Claim 134, comprising in addition an autoantigenic peptide.
137. A pharmaceutical composition for the treatment of an autoimmune disease, comprising a therapeutically effective amount of an isolated copeptide selected from the group consisting of
- | | | | |
|----------------|--|----------------|----------------|
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| SEQ ID NO: 8, | SEQ ID NO: 9, | SEQ ID NO: 10, | SEQ ID NO: 11, |
| SEQ ID NO: 12, | SEQ ID NO: 13, | SEQ ID NO: 14, | SEQ ID NO: 15, |
| SEQ ID NO: 16, | SEQ ID NO: 17, | SEQ ID NO: 18, | SEQ ID NO: 19, |
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| SEQ ID NO: 40, | SEQ ID NO: 41, | SEQ ID NO: 42, | SEQ ID NO: 43, |
| SEQ ID NO: 45, | SEQ ID NO: 46, | SEQ ID NO: 47, | SEQ ID NO: 48, |
| SEQ ID NO: 49, | SEQ ID NO: 50, | SEQ ID NO: 51, | SEQ ID NO: 52, |
| SEQ ID NO: 53, | SEQ ID NO: 54, | SEQ ID NO: 55, | SEQ ID NO: 56, |
| | | | and |
| SEQ ID NO: 57, | and a pharmaceutically acceptable carrier. | | |

138. A pharmaceutical composition for the treatment of an autoimmune disease, comprising a therapeutically effective amount of an isolated copeptide selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 27, SEQ ID NO: 34, SEQ ID NO: 28 and SEQ ID NO: 41, and a pharmaceutically acceptable carrier.
139. A pharmaceutical composition for the treatment of an autoimmune disease, comprising a therapeutically effective amount of an isolated copeptide selected from the group consisting of SEQ ID NO: 27 and SEQ ID NO: 41.
140. A pharmaceutical composition for the treatment of an autoimmune disease, comprising a therapeutically effective amount of an isolated copeptide selected from the group consisting of SEQ ID NO: 25; SEQ ID NO: 26; SEQ ID NO: 27; and SEQ ID NO: 28, and a pharmaceutically acceptable carrier.
141. A method for treating an autoimmune disease which comprises administering a therapeutically effective amount of a copeptide selected from the group consisting of
- | | | | |
|----------------|----------------|----------------|----------------|
| SEQ ID NO: 4, | SEQ ID NO: 5, | SEQ ID NO: 6, | SEQ ID NO: 7, |
| SEQ ID NO: 8, | SEQ ID NO: 9, | SEQ ID NO: 10, | SEQ ID NO: 11, |
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| SEQ ID NO: 20, | SEQ ID NO: 21, | SEQ ID NO: 22, | SEQ ID NO: 23, |
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| SEQ ID NO: 32, | SEQ ID NO: 33, | SEQ ID NO: 34, | SEQ ID NO: 35, |
| SEQ ID NO: 36, | SEQ ID NO: 37, | SEQ ID NO: 38, | SEQ ID NO: 39, |
| SEQ ID NO: 40, | SEQ ID NO: 41, | SEQ ID NO: 42, | SEQ ID NO: 43, |
| SEQ ID NO: 45, | SEQ ID NO: 46, | SEQ ID NO: 47, | SEQ ID NO: 48, |
| SEQ ID NO: 49, | SEQ ID NO: 50, | SEQ ID NO: 51, | SEQ ID NO: 52, |

SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56,
and
SEQ ID NO: 57.

142. A method for treating an autoimmune disease which comprises administering a therapeutically effective amount of a copeptide selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 27, SEQ ID NO: 34, SEQ ID NO: 28 and SEQ ID NO: 41.
143. A method for treating an autoimmune disease which comprises administering a therapeutically effective amount of a copeptide selected from the group consisting of SEQ ID NO: 27 and SEQ ID NO: 41.
144. A method for treating an autoimmune disease which comprises administering a therapeutically effective amount of a copeptide selected from the group consisting of SEQ ID NO: 25; SEQ ID NO: 26; SEQ ID NO: 27; and SEQ ID NO: 28,
145. The method of any one of Claims 141-144, wherein said copeptide inhibits activation of T cells.
146. The method of any one of Claims 141-144, wherein said copeptide activation of T cell suppression mechanisms.
147. The method of any one of Claims 141-144, wherein said copeptide inhibits activation of T cells responsive to myelin basic protein.
148. The method of any one of Claims 141-144, wherein said copeptide inhibits activation of T cells responsive to collagen type II peptide.

149. The method of any one of Claims 141-144, wherein said copeptide binds to a class II MHC protein.
150. The method of any one of Claims 141-144, wherein said copeptide binds to HLA-DR1.
151. The method of any one of Claims 141-144, wherein said copeptide binds to HLA-DR2.
152. The method of any one of Claims 141-144, wherein said copeptide binds to HLA-DR4.
153. The method of any one of Claims 141-144, wherein said copeptide binds to an antigen presenting cell.
154. The method of any one of Claims 141-144, wherein said autoimmune disease is autoimmune hemolytic anemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, chronic immune thrombocytopenic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, multiple sclerosis, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis, or systemic lupus erythematosus.
155. An isolated nucleic acid encoding a copeptide consisting essentially of
- | | | | |
|----------------|----------------|----------------|----------------|
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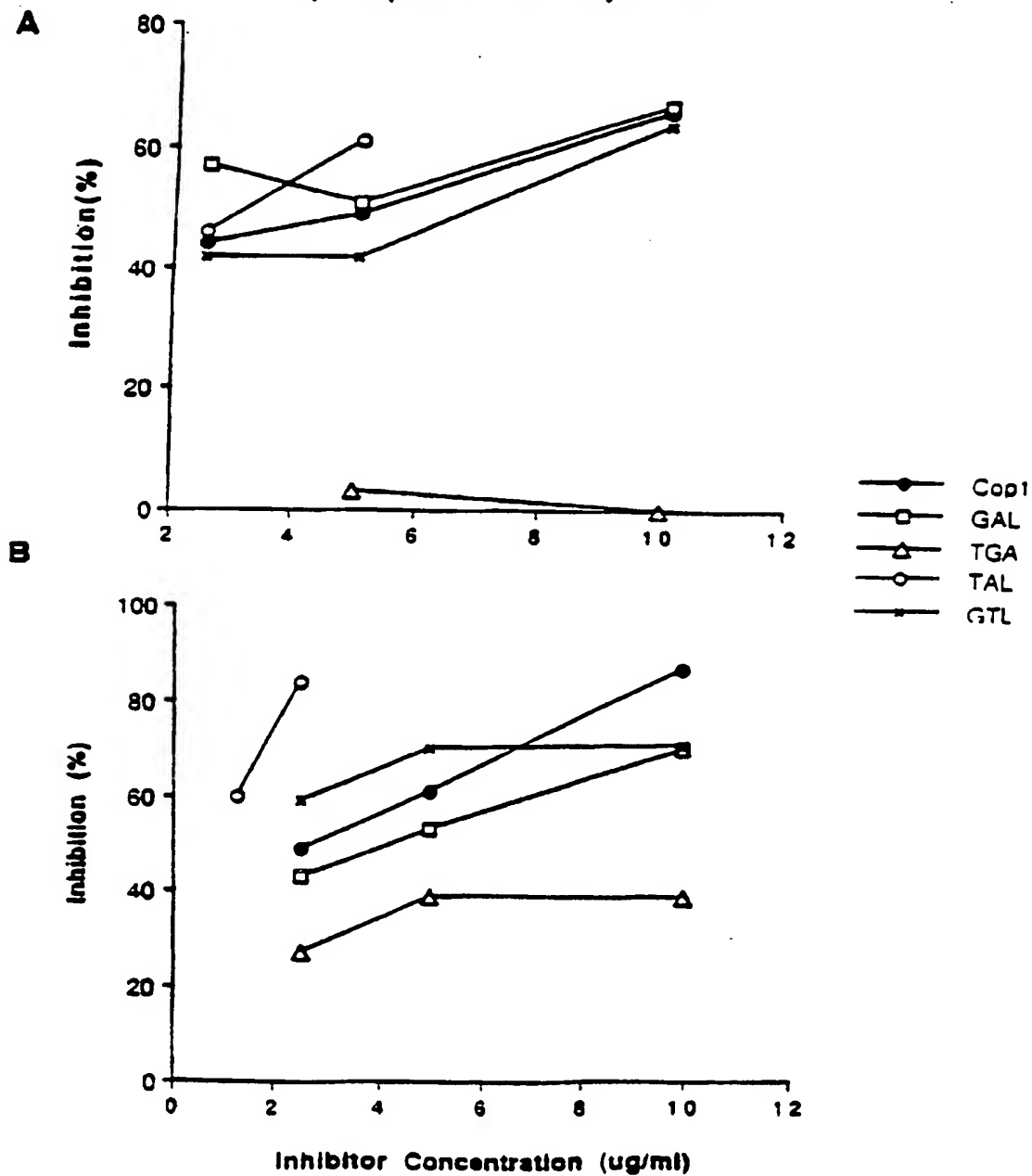
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SEQ ID NO: 49,	SEQ ID NO: 50,	SEQ ID NO: 51	SEQ ID NO: 52
SEQ ID NO: 53,	SEQ ID NO: 54,	SEQ ID NO: 55	SEQ ID NO: 56
or	SEQ ID NO: 57.		

156. A method of anyone of claims 40 or 45 wherein said autoimmune disease is rheumatoid arthritis.

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FIG. 1

Inhibition of MBP 84-102 Specific T cell Response by Cop1-related Polymers



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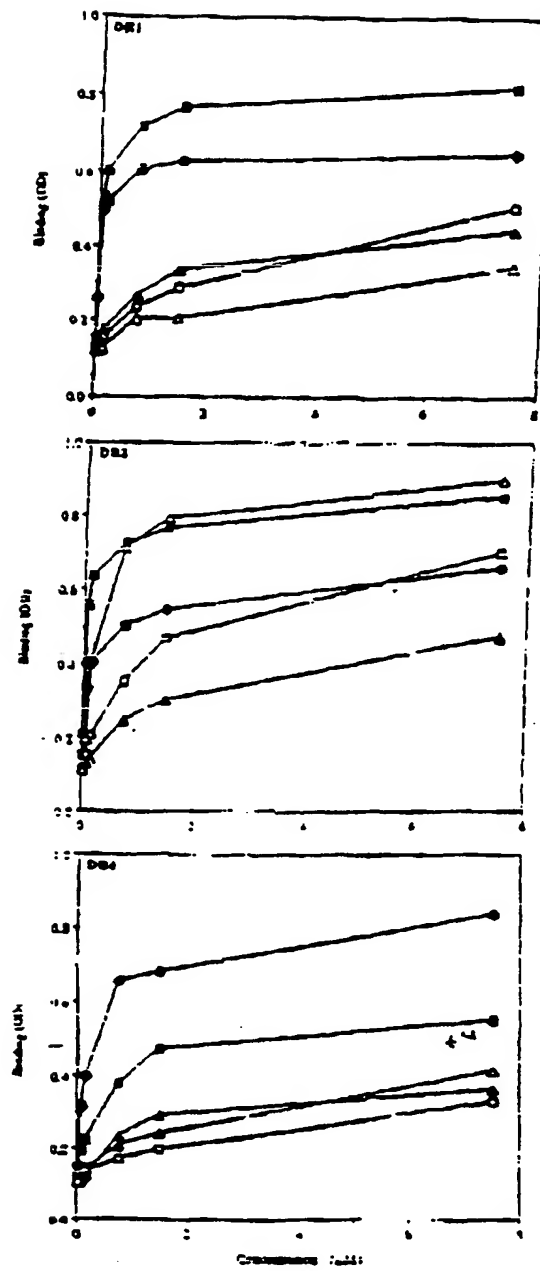


Figure 2A

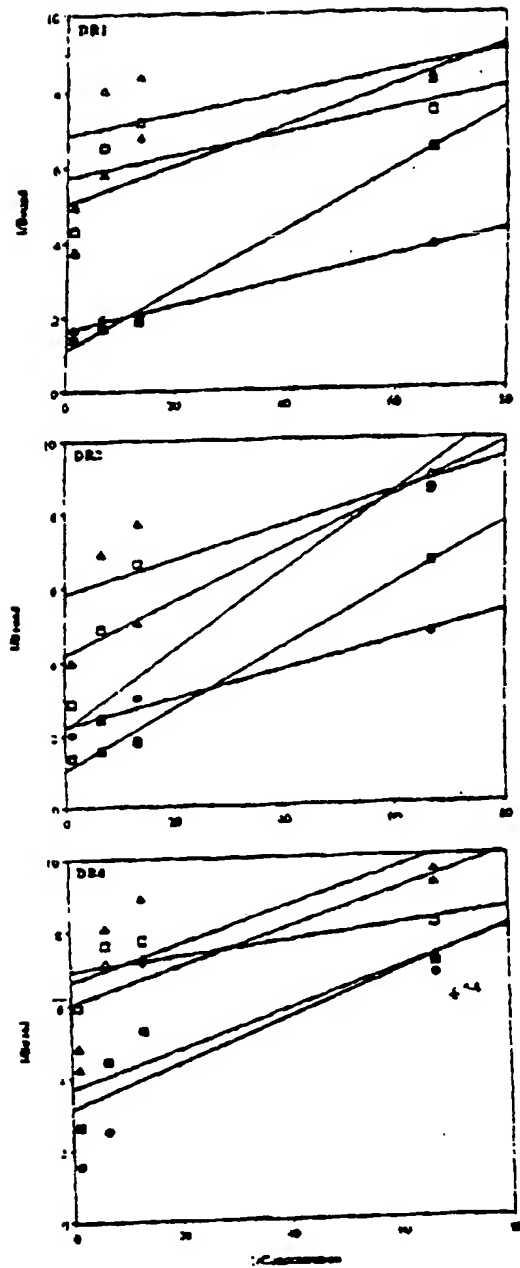


Figure 2B

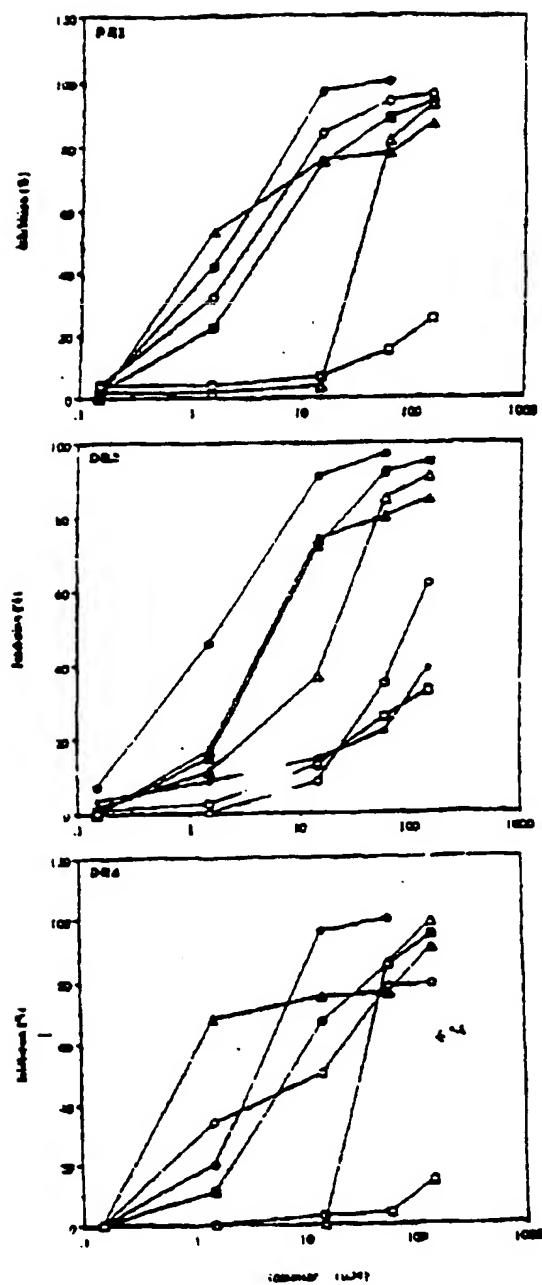
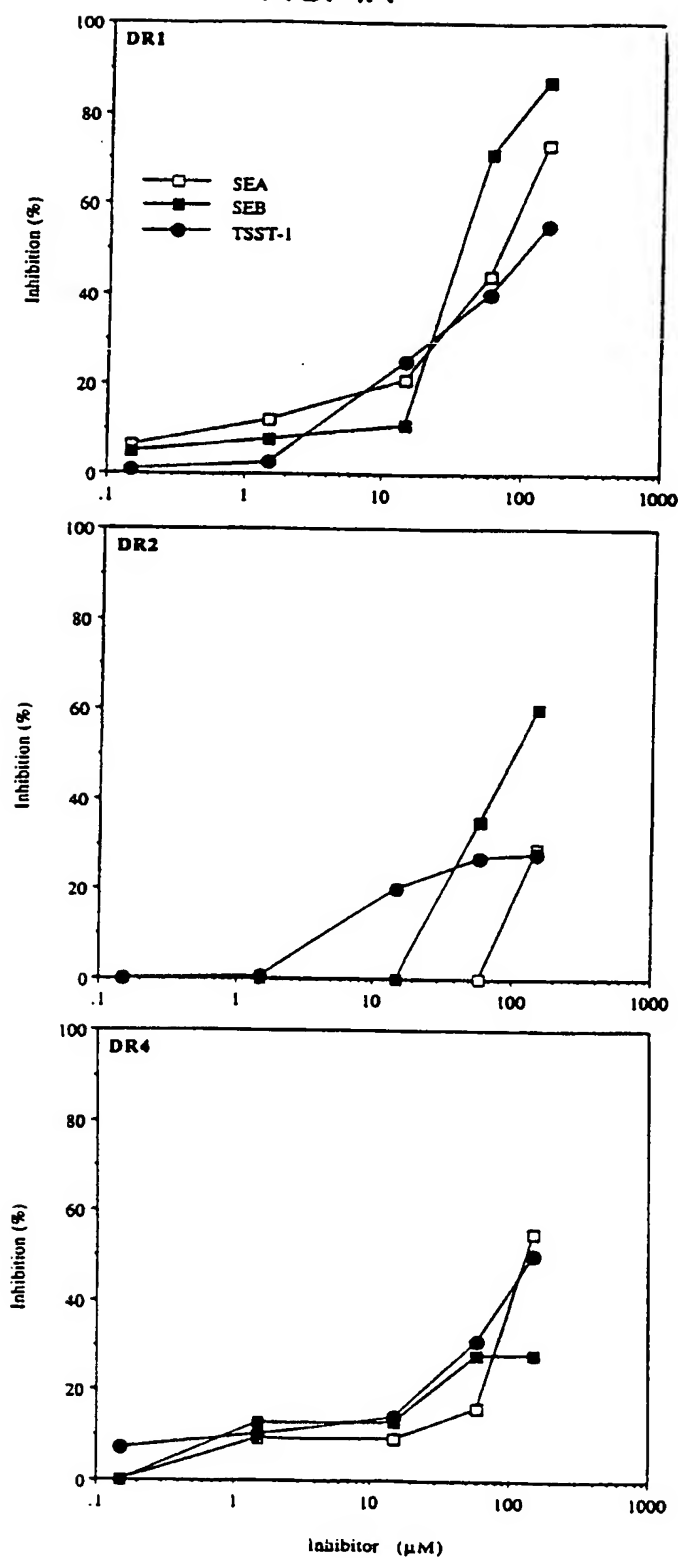


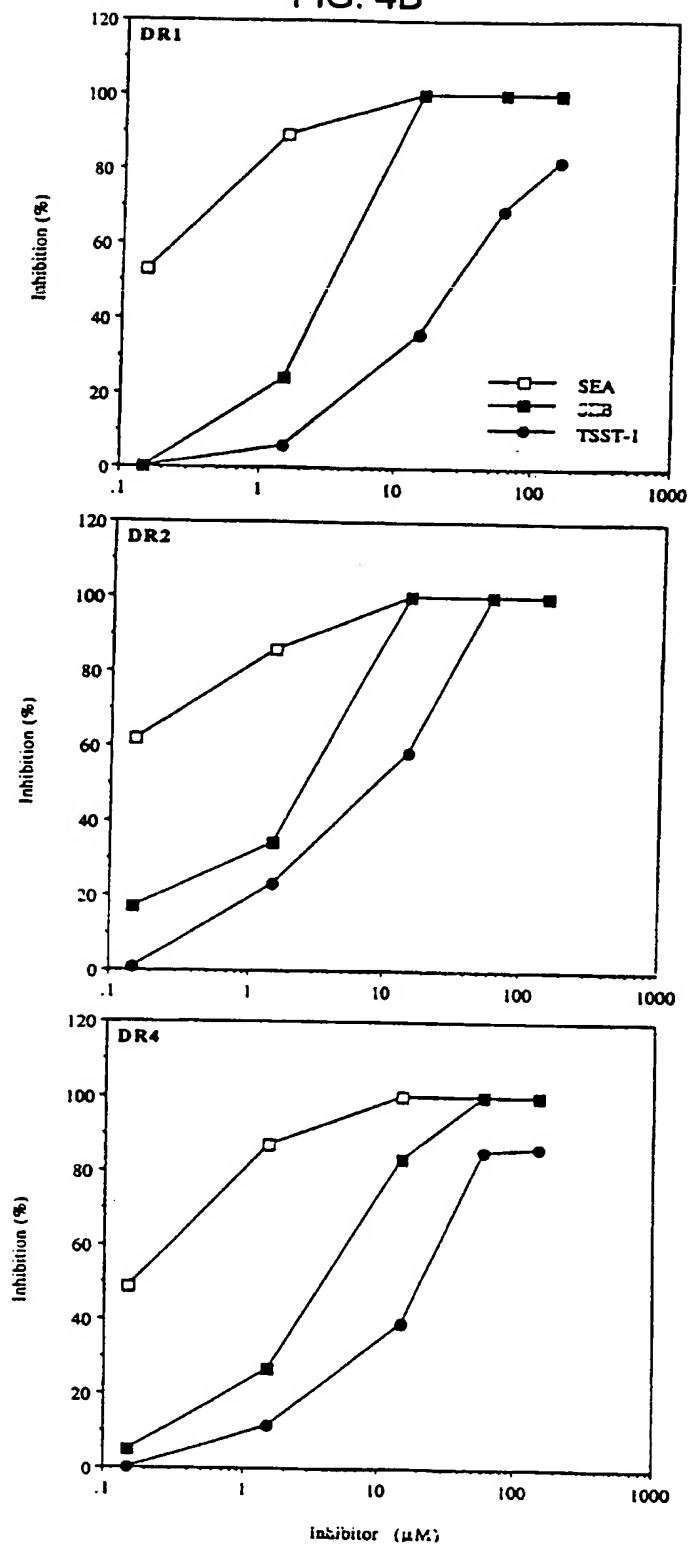
Figure 3

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FIG. 4A

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FIG. 4B



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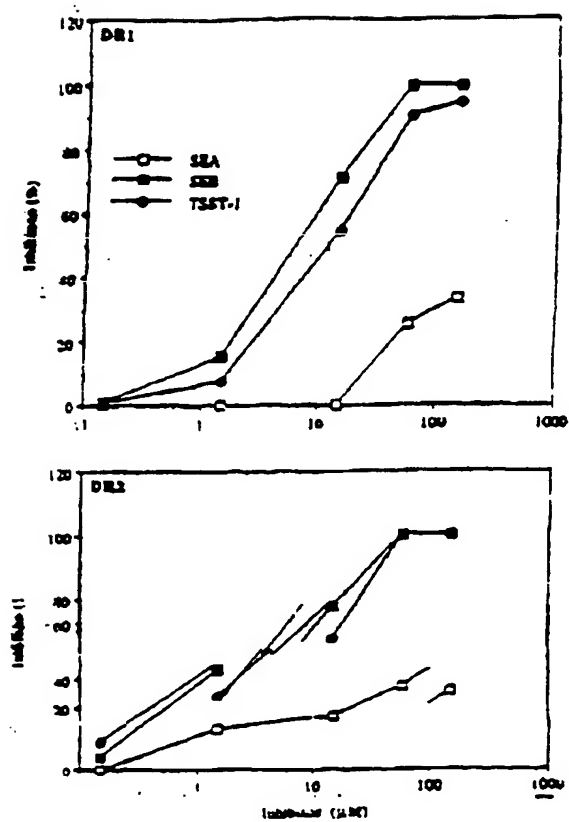
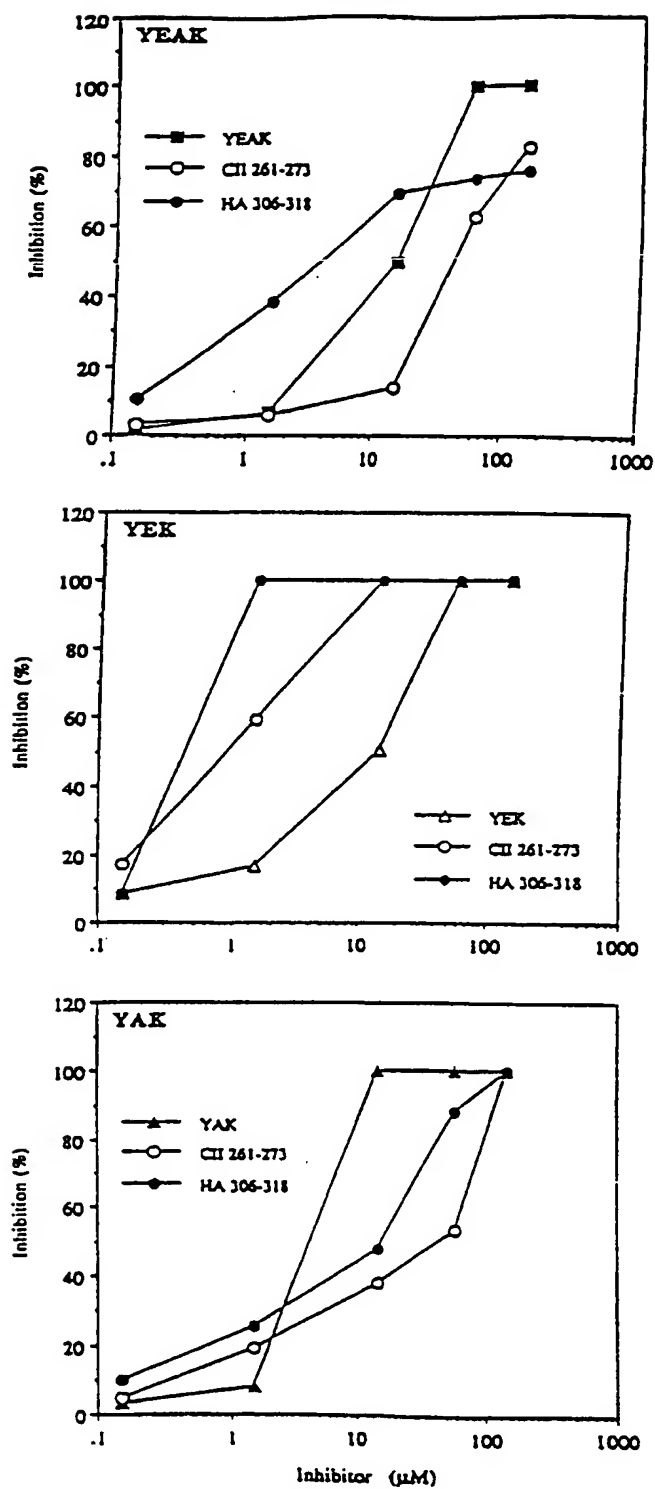


Figure 4C

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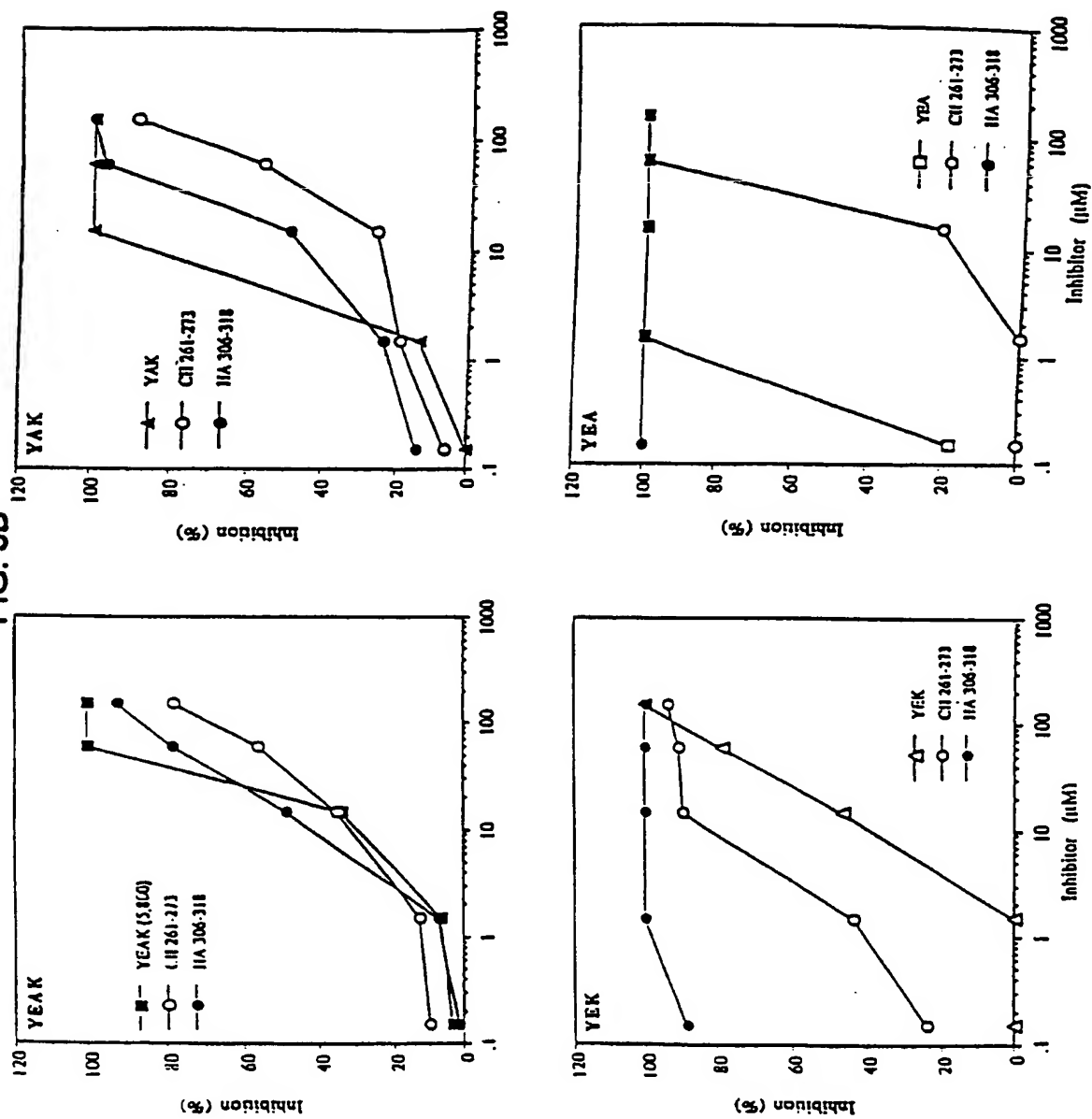
FIG. 5A



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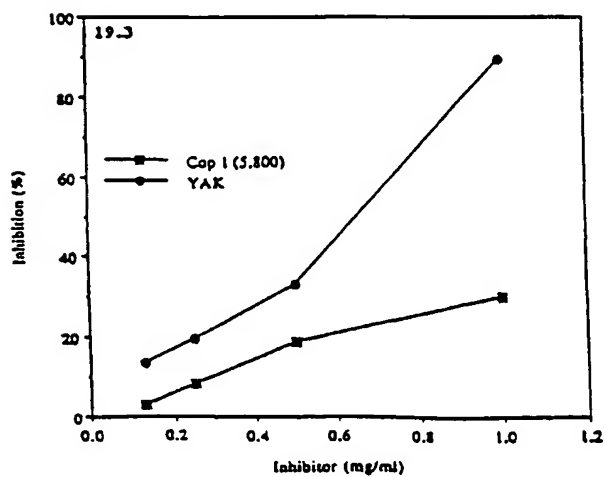
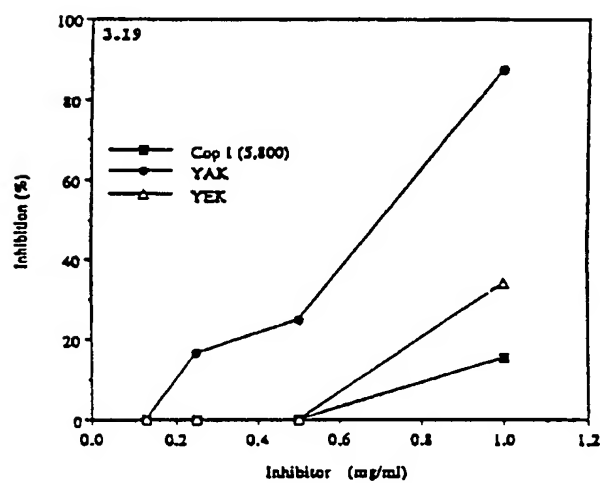
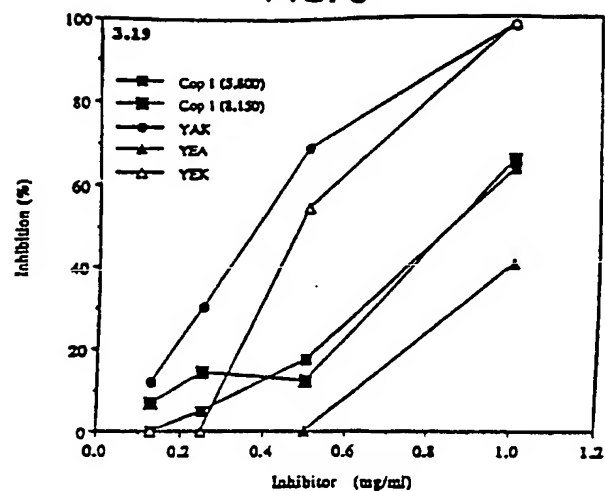
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FIG. 5B



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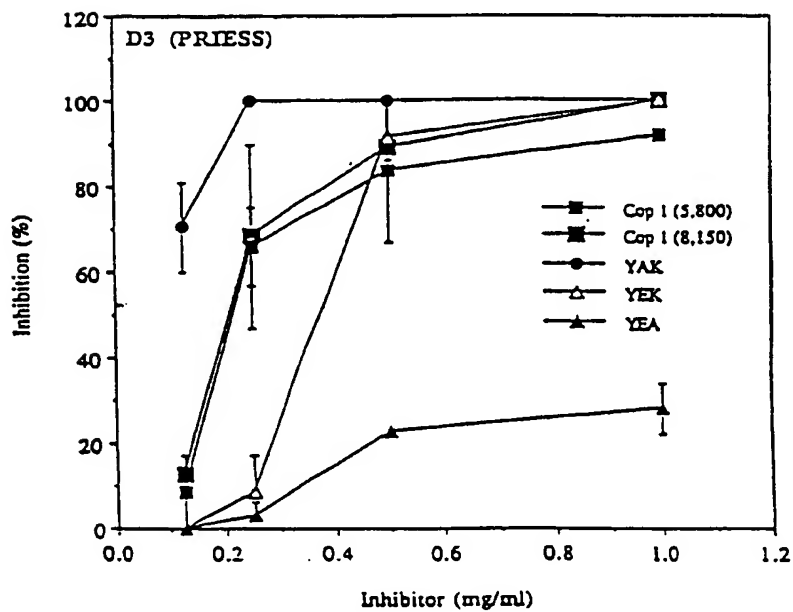
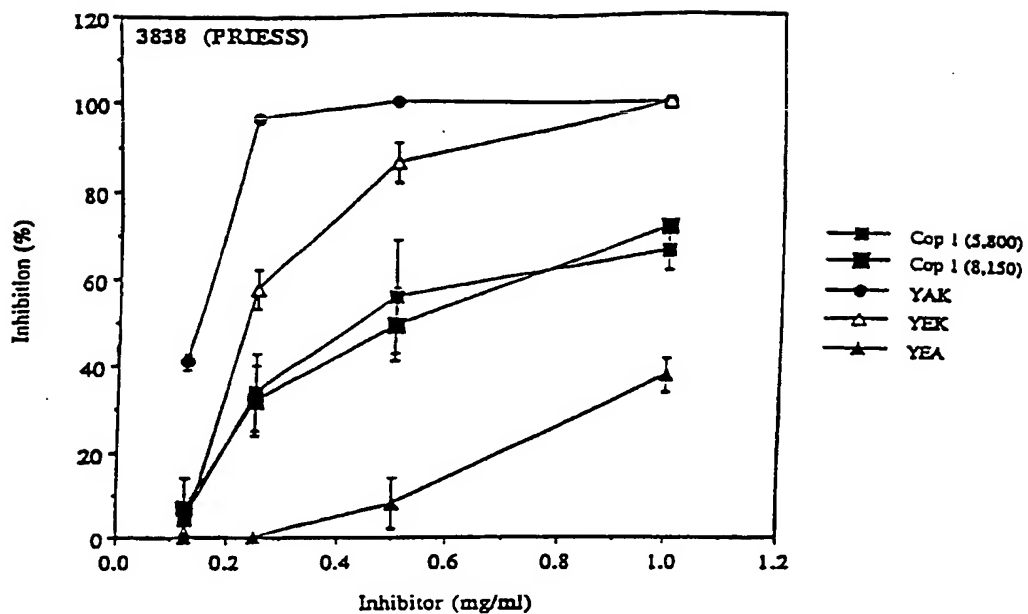
FIG. 6



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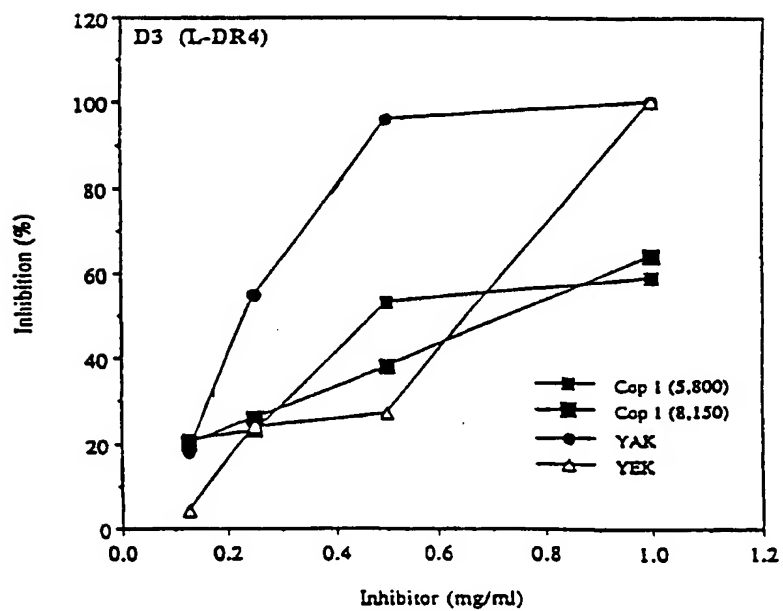
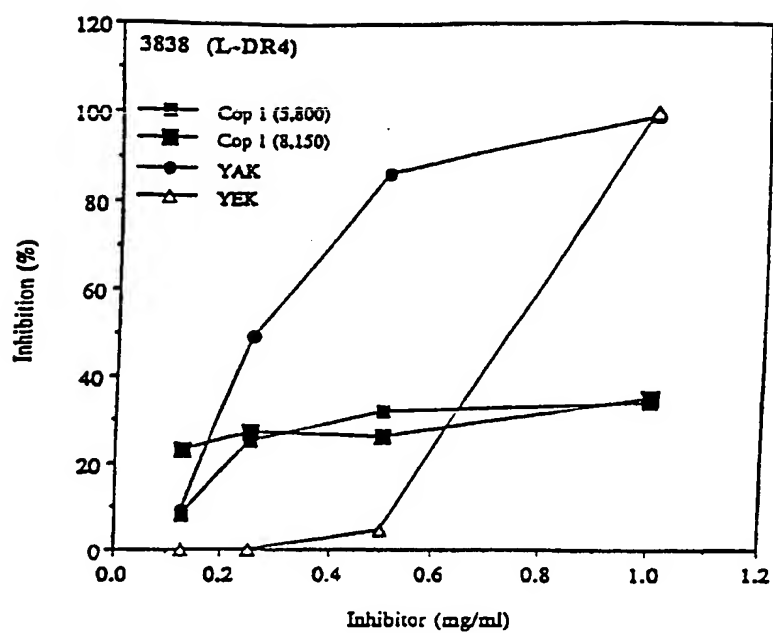
FIG. 7A



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FIG. 7B



SEQUENCE LISTING

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Teitelbaum, Dvora
Arnon, Ruth
Sela, Michael
Fridkis-Harelli, Masha
Strominger, Jack

<120> Treatment of Autoimmune Conditions with Copolymer 1
and Related Copolymers and Peptides

<130> 1662/493762

<140> filed herewith

<141> 1999-07-23

<150> US 60/093,859

<151> 1998-07-23

<150> US 60/101,825

<151> 1998-09-25

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Thr Pro Pro
19

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1 5

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1 4

<210> 15

<211> 4

<212> PRT

<213> Artificial Sequence

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<400> 15

Lys Val Ala Ala

1 4

<210> 16

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<400> 16

Lys Lys Val Ala

1 4

<210> 17

<211> 4

<212> PRT

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<400> 17

Lys Phe Ala Ala

1 4

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<211> 4

<212> PRT

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<400> 18

Lys Lys Phe Ala

1 4

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<211> 5

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5

10

15

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/16747

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C07K 7/00

US CL : 530/300

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/300

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
none

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STNCAS ONLINE, WEST/BRS,
search terms: copolymer 1, TAL, copaxone

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X - Y	Teitelbaum, D. et al. Synthetic Copolymer 1 Inhibits Human T-Cell Lines Specific for Myelin Basic Protein. January 1992, Vol. 89, pages 137-141, especially page 137, paragraph one.	1 --- 2,3,4

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* "A" "B" "L" "O" "P"	Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance earlier document published on or after the international filing date document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) document referring to an oral disclosure, use, exhibition or other means document published prior to the international filing date but later than the priority date claimed	"T" "X" "Y" "A"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art document member of the same patent family
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Date of the actual completion of the international search

14 OCTOBER 1999

Date of mailing of the international search report

29 OCT 1999

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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AMY DECLoux

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/16747

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-4

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/16747

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid. The International application does not comply with the requirements of unity of invention (Rules 13.1, 13.2, and 13.3) for the reasons listed below;

Unity is lacking because claim 59 (of the seventh invention), which is drawn to a synthetic peptide having an amino acid sequence comprising at least three amino acids selected from the group of amino acids consisting of aromatic amino acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids, wherein the synthetic peptide is at least seven amino acids residues in length and is capable of binding to an MHC class II protein associated with autoimmune disease, lacks a special technical feature that distinguishes it over the prior art as shown by the article "Human T-cell response to myelin basic protein peptide (83-89): extensive heterogeneity in antigen recognition, function, and phenotype", by Hemmer et al, Neurology 49:116-1126, Oct 1997. This article describes a synthetic peptide of 17 residues that is restricted by MHC class II protein HLA DR2 and is associated with the autoimmune disease of multiple sclerosis. The sequence of this 17mer peptide is ENPVVHFFKNIVTPRTP and thus encompasses at least three amino acids selected from the group of amino acids consisting of aromatic amino acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids. Therefore, the instant invention lacks Unity of Invention.

Unity is lacking because claim 1 of the first invention, drawn to a terpolymer consisting essentially of tyrosine, alanine and lysine randomly polymerized into a polypeptide, lacks a special technical feature that distinguishes it over the prior art as shown by the article "Copolymer 1 From the Laboratory to the FDA, by Teitelbaum et al, Isr. J. Med. Sci., 1997, Apr.:33(4):280-4. This article describes the effect of Copolymer 1 on experimental allergic encephalomyelitis (EAE) and multiple sclerosis (Conclusions on pg 283 and entire article). Copolymer 1 is a synthetic amino acid copolymer composed of L-alanine, L-lysine, L-glutamic acid and L-tyrosine (page 280, third paragraph, entire article). Since the claim language of "consisting essentially of" is open, the terpolymer of the instant claim reads on the copolymer 1 described in this article. Therefore, the instant invention lacks Unity of Invention.

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1,2,3,4, drawn to a terpolymer, consisting essentially of tyrosine, alanine and lysine,
Group II, claim(s) 5-8, drawn to a terpolymer, consisting essentially of tyrosine, glutamic acid and lysine,
Group III, claim(s) 9-12, drawn to a terpolymer, consisting essentially of glutamic acid, alanine and lysine,
Group IV, claim(s) 13-15, drawn to a terpolymer, consisting essentially of glutamic acid, alanine and tyrosine,
Group V, claim(s) 16-39, drawn to a pharmaceutical composition for the treatment of an autoimmune disease, comprising a terpolymer comprising three amino acids selected from the group of TYR, GLU, ALA, or LYS.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid.

This application contains claims directed to the following species of Group V drawn to a pharmaceutical composition comprising terpolymers. Therefore, a species election is required from terpolymers consisting essentially of one of the following groups of amino acids:

- 1) Tyr Ala Lys,
- 2) Glu Tyr Lys,
- 3) Glu Ala Lys, or
- 4) Tyr Glu Ala.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 17 encompasses species 1, Claim 21 encompasses species 2, claim 25 encompasses species 3 and claim 29 encompasses species 4. The following claims are generic: 17, 21, 25 and 29, for example.

This application contains claims directed to the following species of Group V drawn to a pharmaceutical composition comprising terpolymers for treatment of an autoimmune disease. Therefore, in addition to the species election above, a further species election is required from the following autoimmune conditions;

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- 1) a B Cell mediated autoimmune disease,
- 2) a T Cell mediated autoimmune disease,
- 3) an arthritic condition,
- 4) a demyelinating disease,
- 5) an inflammatory disease,
- 6) multiple sclerosis,
- 7) autoimmune hemolytic anemia,
- 8) autoimmune oophoritis,
- 9) autoimmune thyroiditis,
- 10) autoimmune uveoretinitis,
- 11) chronic immune thrombocytopenic purpura,
- 12) colitis,
- 13) contact sensitivity disease,
- 14) diabetes mellitus,
- 15) Guillain-Barre's Disease,
- 16) Hashimoto's Disease,
- 17) Graves Disease,
- 18) idiopathic myxedema,
- 19) myasthenia gravis,
- 20) psoriasis,
- 21) pemphigus vulgaris,
- 22) rheumatoid arthritis, or
- 23) systemic lupus erythematosus.

These species are distinct because the pathological conditions differ in etiologies and therapeutic endpoints.

The claims are deemed to correspond to the species listed above in the following manner: Claim 34 is drawn to species 1, Claim 35 is drawn to species 2, Claim 36 is drawn to species 3, Claim 37 is drawn to species 4, Claim 38 is drawn to species 5, Claim 39 is drawn to species 6, Claim 39 is drawn to species 7, Claim 39 is drawn to species 8, Claim 39 is drawn to species 9, Claim 39 is drawn to species 10, Claim 39 is drawn to species 11, Claim 39 is drawn to species 12, Claim 39 is drawn to species 13, Claim 39 is drawn to species 14, Claim 39 is drawn to species 15, Claim 39 is drawn to species 16, Claim 39 is drawn to species 17, Claim 39 is drawn to species 18, Claim 39 is drawn to species 19, Claim 39 is drawn to species 20, Claim 39 is drawn to species 21, Claim 39 is drawn to species 22, and Claim 39 is drawn to species 1. The following claims are generic: 34-39, for example.

Group VI, claim(s) 40-58, and 156, drawn to a method of treating autoimmune disease.

This application contains claims directed to the following species of Group VI drawn to a method of treating autoimmune disease using terpolymer polypeptides. If group VI is selected, then a species election is required from terpolymers consisting essentially of the following:

- 1) Tyr, Ala Lys,
- 2) Glu Tyr, Lys, or
- 3) Glu, Ala, Lys.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 41 encompasses species 1, Claim 42 encompasses species 2, Claim 43 encompasses species 3. The following claims are generic: 41-43, for example.

This application contains claims directed to the following species of Group VI drawn to a method of treating autoimmune disease using terpolymers polypeptides. If group VI is selected, then a further species election is required wherein said polypeptide does the following:

- 1) inhibits activation of T cells,
- 2) activates T cell suppressor mechanisms,
- 3) inhibits activation of T cells responsive to myelin basic protein, or
- 4) inhibits activation of T cells responsive to collagen type II peptide.

These species are different methods requiring different process steps and/or endpoints.

The claims are deemed to correspond to the species listed above in the following manner: claim 46 encompasses species 1, claim 47 encompasses species 2, claim 48 encompasses species 3, and claim 49 encompasses species 4. The following claims are generic: 46-49, for example.

This application contains claims directed to the following species of Group VI drawn to a method of treating

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autoimmune disease using terpolymers polypeptides that bind to a class II MHC protein. If group VI is selected, then a further species election is required from the following class II proteins;

- 1) HLA-DR1,
- 2) HLA-DR2, or
- 3) HLA-DR4.

These species are distinct with respect to their structure and sequence and a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 51 encompasses species 1, claim 52 encompasses species 2, and claim 53 encompasses species 3. The following claims are generic: 51-53, for example.

This application contains claims directed to the following species of Group VI drawn to a method of treating autoimmune disease using terpolymers polypeptides that bind to a class II MHC protein. If group VI is selected, then a further species election is required from the following autoimmune diseases;

- 1) multiple sclerosis,
- 2) autoimmune hemolytic anemia,
- 3) autoimmune oophoritis,
- 4) autoimmune thyroiditis,
- 5) autoimmune uveoretinitis,
- 6) chronic immune thrombocytopenic purpura,
- 7) colitis,
- 8) contact sensitivity disease,
- 9) diabetes mellitus,
- 10) Guillain-Barre's Disease,
- 11) Hashimoto's Disease,
- 12) Graves Disease,
- 13) idiopathic myxedema,
- 14) myasthenia gravis,
- 15) psoriasis,
- 16) pemphigus vulgaris,
- 17) rheumatoid arthritis, or
- 18) systemic lupus erythematosus.

These species are distinct because the pathological conditions differ in etiologies and therapeutic endpoints.

The claims are deemed to correspond to the species listed above in the following manner: Claim 55 encompasses species 1, and claim 56 encompasses species 2-18. The following claims are generic: 55-56, for example.

Group VII, claim(s) 59-70, 74-78, drawn to a synthetic peptide having an amino acid sequence comprising at least three amino acids.

This application contains claims directed to the following species of Group VII, drawn to a synthetic peptide having an amino acid sequence comprising at least three amino acids. Therefore, if Group VII is elected, then a species election is required from the following synthetic peptides where:

- 1) the aromatic amino acid is TYR or VAL or PHE,
- 2) the positively charged amino acid is lysine and the sequence comprises LYS-TYR, LYS-VAL, or LYS-PHE,
- 3) the negatively charged amino acid is glutamic acid and the sequence comprises GLU-LYS-TYR or GLU-LYS-VAL or GLU-LYS-PHE,
- 4) where the aliphatic amino acid is ALA and the sequence comprises GLU-LYS-TYR-ALA or GLU-LYS-VAL-ALA, or GLU-LYS-PHE-ALA,
- 5) where the amino terminal amino acid is ALA and the sequence comprises ALA-GLU-LYS-TYR-ALA, or ALA-GLU-LYS-VAL-ALA, or ALA-GLU-LYS-PHE-ALA,
- 6) where the aliphatic amino acid is ALA and the sequence comprises LYS-GLU-TYR-ALA, LYS-TYR-ALA-GLU, LYS-GLU-VAL-ALA, LYS-VAL-ALA-GLU, LYS-GLU-PHE-ALA, OR LYS-PHE-ALA-GLU,
- 7) where the aliphatic amino acid is ALA and the sequence comprises: LYS-TYR-ALA-ALA, LYS-LYS-TYR-ALA, LYS-VAL-ALA-ALA, LYS-LYS-VAL-ALA, LYS-PHE-ALA-ALA, or LYS-LYS-PHE-ALA, or
- 8) where the peptide further comprises two amino acids of ALA and the sequence comprises: ALA-LYS-TYR-ALA-GLU, GLU-ALA-LYS-TYR-ALA-ALA, LYS-VAL-ALA-GLU, GLU-ALA-LYS-VAL-ALA, ALA-LYS-PHE-ALA-GLU, OR GLU-ALA-LYS-PHE-ALA.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claims 60-67 encompass species 1-8 respectively. The following claims are generic: 60-67, for example.

This application contains claims directed to the following sub-species of species 1 above. Therefore, if species 1 is elected, then a sub-species election is required from terpolymers consisting essentially of the following;

- 1) aromatic amino acid is tyrosine
- 2) aromatic amino acid is valine, or
- 3) aromatic amino acid is phenylalanine.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 60 encompasses species 1 and is generic.

This application contains claims directed to the following sub-species of species 2 above. Therefore, if species 2 is elected, then a sub-species election is required from terpolymers consisting essentially of a positively charged amino acid, Lysine, and the sequence comprises the following;

- 1) LYS-TYR,
- 2) LYS-VAL, or
- 3) LYS-PHE.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 61 encompasses species 2 and is generic.

This application contains claims directed to the following sub-species of species 3 above. Therefore, if species 3 is elected, then a sub-species election is required from terpolymers consisting essentially of a negatively charged amino acid, Glutamate (GLU), and the sequence comprises the following;

- 1) GLU-LYS-TYR,
- 2) GLU-LYS-VAL, or
- 3) GLU-LYS-PHE.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 62 encompasses species 3 and is generic.

This application contains claims directed to the following sub-species of species 4 above. Therefore, if species 4 is elected, then a sub-species election is required from terpolymers consisting essentially of an aliphatic amino acid, Alanine (ALA), and the sequence comprises the following;

- 1) GLU-LYS-TYR-ALA
- 2) GLU-LYS-VAL-ALA, OR
- 3) GLU-LYS-PHE-ALA.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 63 encompasses species 4 and is generic.

This application contains claims directed to the following sub-species of species 5 above. Therefore, if species 5 is elected, then a sub-species election is required from terpolymers where the amino terminal amino acid is Alanine (ALA), and the sequence comprises the following;

- 1) ALA-GLU-LYS-TYR-ALA,
- 2) ALA-GLU-LYS-VAL-ALA, OR
- 3) ALA-GLU-LYS-PHE-ALA.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 64 encompasses species 5 and is generic.

This application contains claims directed to the following sub-species of species 6 above. Therefore, if species 6 is elected, then a sub-species election is required from terpolymers where the aliphatic amino acid is Alanine (ALA), and the sequence comprises the following;

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- 1) LYS-GLU-TYR-ALA,
- 2) LYS-TYR-ALA-GLU,
- 3) LYS-GLU-VAL-ALA,
- 4) LYS-VAL-ALA-GLU,
- 5) LYS-GLU-PHE-ALA, OR
- 6) LYS-PHE-ALA-GLU.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 65 encompasses species 6 and is generic.

This application contains claims directed to the following sub-species of species 7 above. Therefore, if species 7 is elected, then a sub-species election is required from terpolymers where the aliphatic amino acid is ALA, and the sequence comprises one of the following;

- 1) LYS-TYR-ALA-ALA,
- 2) LYS-LYS-TYR-ALA,
- 3) LYS-VAL-ALA-ALA,
- 4) LYS-LYS-VAL-ALA,
- 5) LYS-PHE-ALA-ALA, OR
- 6) LYS, LYS, PHE, ALA.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 66 encompasses species 7 and is generic.

This application contains claims directed to the following sub-species of species 8 above. Therefore, if species 8 is elected, then a sub-species election is required from terpolymers where the peptide further comprises two amino acids of ALA, and the sequence comprises the following;

- 1) ALA-LYS-TYR-ALA-GLU,
- 2) GLU-ALA-LYS-TYR-ALA,
- 3) ALA-LYS-VAL-ALA-GLU,
- 4) GLU-ALA-LYS-VAL-ALA,
- 5) ALA-LYS-PHE-ALA-GLU, OR
- 6) GLU-ALA-LYS-PHE-ALA

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: claim 67 encompasses species 8 and is generic.

This application contains claims directed to the following species of Group VII, drawn to a synthetic peptide having an amino acid sequence comprising at least three amino acids. Therefore, if Group VII is elected, then a further species election is required from the following synthetic peptides where the peptide length is as follows:

- 1) 7-25 amino acids,
- 2) 7-15 amino acids, or
- 3) 7-100 amino acids.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 74 is 7-25 amino acids, Claim 70 is 7-10 amino acids, and Claim 75 is 7-15 amino acids. The following claims are generic: 70, 74, and 75, for example.

Group VIII, claim(s) 71-73, 79, drawn to therapeutic peptide.

This application contains claims directed to the following species of Group VIII, drawn to a therapeutic peptide. Therefore, if Group VIII is elected, then a species election is required wherein the peptide has at least one of GLU, LYS and ALA and an amino acid from the following;

- 1) TYR,
- 2) VAL, or
- 3) PHE.

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These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claim 71 is deemed to correspond to the species listed above and is generic, for example.

This application contains claims directed to the following species of Group VIII, drawn to a therapeutic peptide. Therefore, if Group VIII is elected, then a further species election is required wherein the length of the peptide is as follows:

- 1) 7-100 Amino Acids or
- 2) 7-50 Amino Acids.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 72 encompasses 7-100 Amino Acids. Claim 73 encompasses 7-50 Amino Acids. The following claims are generic: 72 and 73, for example.

Group IX, claim(s) 80 and 81 drawn to an isolated peptide.

This application contains claims directed to the following species of Group IX, drawn to a therapeutic peptide. Therefore, if Group IX is elected, then a species election is required from an isolated peptide having a sequence of one of the following:

- 1) SEQ ID NO:25,
- 2) SEQ ID NO:26,
- 3) SEQ ID NO:27,
- 4) SEQ ID NO:28,
- 5) AKEVAAAAAAAAKAAAA,
- 6) AKEFAAAAAAAAAKAAAA,
- 7) AAEVAAAAAAAAKAAAA,
- 8) AAEFAAAAAAAAKAAAA,
- 9) AAKVAEAAAAAAAAKAAAA,
- 10) AAKFAEAAAAAAAAKAAAA,
- 11) EAKVAAAAAAAAKAAAA, OR
- 12) EAKFAAAAAAAAAKAAAA.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 80 encompasses species 1-4, Claim 81 encompasses species 5-12. The following claims are generic: 80 and 81.

Group X, claim(s) 82 and 83 drawn to an isolate peptide.

This application contains claims directed to the following species of Group X, drawn to a therapeutic peptide. Therefore, if Group X is elected, then a species election is required from an isolated peptide having a sequence of the following:

- 1) SEQ ID NO:29,
- 2) SEQ ID NO:25,
- 3) SEQ ID NO:30,
- 4) SEQ ID NO:31,
- 5) SEQ ID NO:26,
- 6) SEQ ID NO:32,
- 7) SEQ ID NO:33,
- 8) SEQ ID NO:27,
- 9) SEQ ID NO:34,
- 10) SEQ ID NO:35,
- 11) SEQ ID NO:28,
- 12) SEQ ID NO:37,
- 13) SEQ ID NO:38,
- 14) SEQ ID NO:39,
- 15) SEQ ID NO:40,
- 16) SEQ ID NO:41,
- 17) SEQ ID NO:42,
- 18) SEQ ID NO:43,
- 19) SEQ ID NO:29, wherein Y is substituted with V,

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20) SEQ ID NO:25, wherein Y is substituted with V,
21) SEQ ID NO:30, wherein Y is substituted with V,
22) SEQ ID NO:31, wherein Y is substituted with V,
23) SEQ ID NO:26, wherein Y is substituted with V,
24) SEQ ID NO:32, wherein Y is substituted with V,
25) SEQ ID NO:33, wherein Y is substituted with V,
26) SEQ ID NO:27, wherein Y is substituted with V,
27) SEQ ID NO:34, wherein Y is substituted with V,
28) SEQ ID NO:35, wherein Y is substituted with V,
29) SEQ ID NO:28, wherein Y is substituted with V,
30) SEQ ID NO:37, wherein Y is substituted with V,
31) SEQ ID NO:38, wherein Y is substituted with V,
32) SEQ ID NO:39, wherein Y is substituted with V,
33) SEQ ID NO:40, wherein Y is substituted with V,
34) SEQ ID NO:41, wherein Y is substituted with V,
35) SEQ ID NO:42, wherein Y is substituted with V,
36) SEQ ID NO:43, wherein Y is substituted with V,
37) SEQ ID NO:29, wherein Y is substituted with F,
38) SEQ ID NO:25, wherein Y is substituted with F,
39) SEQ ID NO:30, wherein Y is substituted with F,
40) SEQ ID NO:31, wherein Y is substituted with F,
41) SEQ ID NO:26, wherein Y is substituted with F,
42) SEQ ID NO:32, wherein Y is substituted with F,
43) SEQ ID NO:33, wherein Y is substituted with F,
44) SEQ ID NO:27, wherein Y is substituted with F,
45) SEQ ID NO:34, wherein Y is substituted with F,
46) SEQ ID NO:35, wherein Y is substituted with F,
47) SEQ ID NO:28, wherein Y is substituted with F,
48) SEQ ID NO:37, wherein Y is substituted with F,
49) SEQ ID NO:38, wherein Y is substituted with F,
50) SEQ ID NO:39, wherein Y is substituted with F,
51) SEQ ID NO:40, wherein Y is substituted with F,
52) SEQ ID NO:41, wherein Y is substituted with F,
53) SEQ ID NO:42, wherein Y is substituted with F, OR
54) SEQ ID NO:43, wherein Y is substituted with F.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 82 encompasses species 1-18. Claim 83 encompasses species 19-54. The following claims are generic: 82 and 83, for example.

Group XI, claim(s) 84-90, drawn to an isolated peptide composition having an amino acid sequence capable of inhibiting an immune response in a subject to an autoantigen.

This application contains claims directed to the following species of Group XI, drawn to a therapeutic peptide. Therefore, if Group XI is elected, then a species election is required from an isolated peptide having a sequence of one of the following conditions;

- 1) multiple sclerosis, or
- 2) arthritis.

These species are distinct because the pathological conditions differ in etiologies and therapeutic endpoints. The claim 85 is deemed to correspond to the species listed above and is generic.

This application contains claims directed to the following species of Group XI, drawn to a therapeutic peptide that binds to MHC class II proteins. Therefore, if Group XI is elected, then a further species election is required from an isolated peptide having a sequence of the following MHC Class II proteins:

- 1) HLA-DR4,
- 2) HLA-DR1, or
- 3) HLA-D32.

54) SEQ ID NO:43, wherein Y is substituted with F.

These species are distinct with respect to their structure and sequence, a person of ordinary skill in the art

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would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 86 encompasses species 1-2. Claim 87 encompasses species 3. The following claims are generic: 86 and 87, for example.

This application contains claims directed to the following species of Group XI, drawn to a therapeutic peptide that binds to MHC class II proteins wherein the position in the amino acid sequence of the peptide that corresponds to an antigen binding pocket is identified as a particular amino acid. Therefore, if Group XI is elected, then a further species election is required from the following amino acids:

- 1) TYR,
- 2) VAL,
- 3) PHE or
- 4) ALA.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 88 encompasses species 1-3. Claim 89 encompasses species 4. The following claims are generic: 88 and 89, for example.

This application contains claims directed to the following species of Group XI, drawn to a therapeutic peptide that binds to MHC class II proteins wherein the position in the amino acid sequence of the peptide that corresponds to an antigen binding pocket is identified as a particular amino acid that is 8 amino residues beyond the first amino acid of the P1 pocket. Therefore, if Group XI is elected, then a further species election is required from one following amino acids:

- 1) LYS, or
- 2) ALA.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 90 encompasses species 1-2. The following claim is generic: 90, for example.

Group XII, claim(s) 91, drawn to a pharmaceutical composition containing a mixture of two different peptide sequences.

Group XIII, claim(s) 92-113, drawn to a method of treating a subject having autoimmune disease with a synthetic heteropolymer.

This application contains claims directed to the following species of Group XIII, drawn to a method of treating a subject having autoimmune disease with a synthetic heteropolymer where the synthetic heteropolymer is comprised of at least two different amino acids, the first being an amino acid which is charged. Therefore, if Group XIII is elected, then a species election is required from the following charged amino acids:

- 1) LYS,
- 2) GLU, or
- 3) ASP.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 93 encompasses species 1-3. The following claim is generic: 93, for example.

This application contains claims directed to the following species of Group XIII, drawn to a method of treating a subject having autoimmune disease with a synthetic heteropolymer where the synthetic heteropolymer is comprised of at least two different amino acids, the first being an amino acid which is charged and a second being an amino acid which is hydrophobic. Therefore, if Group XIII is elected, then a further species election is required from the following hydrophobic amino acids:

- 1) VAL,
- 2) LEU,
- 3) ILE,
- 4) ALA,
- 5) PHE, or
- 6) TYR.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 95

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encompasses species 1-6. The following claim is generic: 95, for example.

This application contains claims directed to the following species of Group XIII, drawn to a method of treating a subject having autoimmune disease with a synthetic heteropolymer. Therefore, if Group XIII is elected, then a further species election is required from a heteropolymer that comprises the following groups of amino acids;

- 1) LYS,ALA,TYR,
- 2) LYS,GLU,ALA,PHE,
- 3) LYS,GLU,ALA,VAL.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 96 encompasses species 1, claim 97 encompasses species 2, claim 98 encompasses species 3. The following claims are generic: 96-98, for example.

This application contains claims directed to the following species of Group XIII, drawn to a method of treating a subject having autoimmune disease with a synthetic heteropolymer with an additional therapeutic agent. If Group XIII is elected, then a further species election is required from the following therapeutic agents;

- 1) antibody,
- 2) an enzyme inhibitor,
- 3) an anti-bacterial agent,
- 4) an antiviral agent,
- 5) a steroid,
- 6) a non-steroidal anti-inflammatory agent,
- 7) an antimetabolite,
- 8) a cytokine, or
- 9) a soluble cytokine receptor.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 109 encompasses species 1-9 and is generic, for example.

This application contains claims directed to the following sub-species of the species of therapeutic agents of Group XIII. If species 2, enzyme inhibitors, is elected then a further election is required from the following enzyme inhibitors,

- 1) a protease inhibitor, or
- 2) a cyclooxygenase inhibitor.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

Claim 112 encompasses sub-species 1-2 and is generic, for example.

This application contains claims directed to the following sub-species of the species of therapeutic agents of Group XIII. If species 8, cytokines, is elected then a further election is required from the following cytokines;

- 1) interferon-beta,
- 2) interleukin-4, or
- 3) interleukin-10.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

Claim 111 encompasses sub-species 1-3 and is generic, for example.

This application contains claims directed to the following species of Group XIII, drawn to a method of treating a subject having autoimmune disease by administering a synthetic heteropolymer. If Group XIII is elected, then a further species election is required from the following routes of administration;

- 1) intravenous,
- 2) intramuscular,
- 3) intraperitoneal,
- 4) subcutaneous,
- 5) oral, or
- 6) transdermal.

These species are distinct with respect to methods requiring different processes, and a person of ordinary skill

in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 111 encompasses species 1-6 and is generic, for example.

Group XIV, claim(s) 114-120, drawn to a method of making a therapeutic heteropolymer composition.

This application contains claims directed to the following species of Group XIV, drawn to a method of making a therapeutic heteropolymer composition that inhibits the binding of an autoantigen to a MHC Class II peptide. If Group XIV is elected, then a species election is required from the following sets of autoantigen/Class II protein;

- 1) the autoantigen is collagen Type II peptide 261-273 and the MHC class II protein is HLA-DR1,
- 2) the autoantigen is collagen Type II peptide 261-273 and the MHC class II protein is HLA-DR4,
- 3) the autoantigen is myelin basic protein peptide 84-102 and the MHC class II protein is HLA-DR2.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 116 encompasses species 1 and 2, claim 117 is species 3. The following claims are generic: 116-117, for example.

This application contains claims directed to the following species of Group XIV, drawn to a method of obtaining a therapeutic heteropolymer composition that inhibits the binding of an autoantigen to a MHC Class II peptide. If Group XIV is elected, then a species election is required from the following heteropolymers that at a concentration of 1.5 micromolar inhibits 50% binding of the binding of one of the following peptides to a MHC Class II peptide;

- 1) collagen Type II peptide 261-273 at a concentration of at least 20 micromolar, to the MHC class II protein HLA-DR1,
- 2) collagen Type II peptide 261-273 at a concentration of at least 20 micromolar, to the MHC class II protein HLA-DR4,
- 3) myelin basic protein peptide 84-102 at a concentration of at least 20 micromolar, to the MHC class II protein is HLA-DR2.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

Claim 118 is species 1 and 2, claim 119 is species 3. The following claims are generic: 118-119, for example.

Group XV, claim(s) 121-127, drawn to a method of obtaining an MHC class II binding motif amino acid sequence in a mixture of synthetic peptide heteropolymers.

This application contains claims directed to the following species of Group XV, drawn to a method of obtaining a therapeutic heteropolymer composition that inhibits the binding of an autoantigen to a MHC Class II peptide, where the MHC protein is associated with an autoimmune disease. If Group XV is elected, then a species election is required from the following autoimmune diseases;

- 1) arthritic condition, or
- 2) demyelinating condition.

These species are distinct because the pathological conditions differ in etiologies and therapeutic endpoints.

The claims are deemed to correspond to the species listed above in the following manner: Claim 125 encompasses species 1 and 2, and is generic, for example.

Group XVI, claim(s) 128-133, drawn to a method of treating a subject having an arthritic condition with a pure heteropolymer.

This application contains claims directed to the following species of Group XVI, drawn to a method of treating a subject having an arthritic condition with an effective dosage of pure heteropolymer. If Group XVI is elected, then a species election is required from the following dosages;

- 1) 5 mg/day
- 2) 10 mg/day,
- 3) 15 mg/day,
- 4) 20 mg per day, or
- 5) 25-400 mg/day.

These species are distinct with respect to methods requiring different effective dosages, and a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 129 encompasses species 1, claim 130 encompasses species 2, claim 131 encompasses species 3, claim 132 encompasses species 3, claim 133 encompasses species 4 and claim 134 encompasses species 5 and claims 129-134 are generic, for

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example.

Group XVII, claim(s) 134-136, drawn to a kit for assaying the binding of an analyte to an MHC protein.

This application contains claims directed to the following species of Group XVII, drawn to a kit for assaying the binding of an analyte to an MHC Class II protein. If Group XVII is elected, then a species election is required from the following MHC Class II proteins;

- 1) HLA-DR1,
- 2) HLA-DR2, or
- 3) HLA-DR4.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 135 encompasses species 1-3, and is generic, for example.

Group XVIII, claim(s) 137-140, drawn to a pharmaceutical composition for the treatment of an autoimmune disease comprising a therapeutically effective amount of an isolated copeptide.

This application contains claims directed to the following species of Group XVIII, drawn to a pharmaceutical composition comprising a therapeutically effective amount of an isolated copeptide. If Group XVII is elected, then a species election is required from the following isolated copeptides;

- 1) SEQ ID NO:4
- 2) SEQ ID NO:5
- 3) SEQ ID NO:6
- 4) SEQ ID NO:7
- 5) SEQ ID NO:8
- 6) SEQ ID NO:9
- 7) SEQ ID NO:10
- 8) SEQ ID NO:11
- 9) SEQ ID NO:12
- 10) SEQ ID NO:13
- 11) SEQ ID NO:14
- 12) SEQ ID NO:15
- 13) SEQ ID NO:16
- 14) SEQ ID NO:17
- 15) SEQ ID NO:18
- 16) SEQ ID NO:19
- 17) SEQ ID NO:20
- 18) SEQ ID NO:21
- 19) SEQ ID NO:22
- 20) SEQ ID NO:23
- 21) SEQ ID NO:24
- 22) SEQ ID NO:25
- 23) SEQ ID NO:26
- 24) SEQ ID NO:27
- 25) SEQ ID NO:28
- 26) SEQ ID NO:29
- 27) SEQ ID NO:30
- 28) SEQ ID NO:31
- 29) SEQ ID NO:32
- 30) SEQ ID NO:33
- 30) SEQ ID NO:34
- 31) SEQ ID NO:35
- 32) SEQ ID NO:36
- 33) SEQ ID NO:37
- 34) SEQ ID NO:38
- 35) SEQ ID NO:39
- 36) SEQ ID NO:40
- 37) SEQ ID NO:41
- 38) SEQ ID NO:42

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- 39) SEQ ID NO:43
- 40) SEQ ID NO:44
- 41) SEQ ID NO:45
- 42) SEQ ID NO:46
- 43) SEQ ID NO:47
- 44) SEQ ID NO:48
- 45) SEQ ID NO:49
- 46) SEQ ID NO:50
- 47) SEQ ID NO:51
- 48) SEQ ID NO:52
- 49) SEQ ID NO:53
- 50) SEQ ID NO:54
- 51) SEQ ID NO:55
- 52) SEQ ID NO:56 or,
- 53) SEQ ID NO:57.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 137 encompasses species 1-53, claim 138 encompasses species 50, 23, 30 and 24 and 37, claim 139 encompasses species 23 and 37, and claim 140 encompasses species 21, 22, 23 and 24. Claims 137, 138, 139 and 140 are generic.

Group XIX, claim(s) 141-154, drawn to a method of treating an autoimmune disease which comprises administering a therapeutically effective amount of an isolated copeptide.

This application contains claims directed to the following species of Group XIX, drawn to a method of treating an autoimmune disease which comprises administering an therapeutically effective amount of an isolated copeptide. If Group XIX is elected, then a species election is required from the following isolated copeptides;

- 1) SEQ ID NO:4
- 2) SEQ ID NO:5
- 3) SEQ ID NO:6
- 4) SEQ ID NO:7
- 5) SEQ ID NO:8
- 6) SEQ ID NO:9
- 7) SEQ ID NO:10
- 8) SEQ ID NO:11
- 9) SEQ ID NO:12
- 10) SEQ ID NO:13
- 11) SEQ ID NO:14
- 12) SEQ ID NO:15
- 13) SEQ ID NO:16
- 14) SEQ ID NO:17
- 15) SEQ ID NO:18
- 16) SEQ ID NO:19
- 17) SEQ ID NO:20
- 18) SEQ ID NO:21
- 19) SEQ ID NO:22
- 20) SEQ ID NO:23
- 21) SEQ ID NO:24
- 22) SEQ ID NO:25
- 23) SEQ ID NO:26
- 24) SEQ ID NO:27
- 25) SEQ ID NO:28
- 26) SEQ ID NO:29
- 27) SEQ ID NO:30
- 28) SEQ ID NO:31
- 29) SEQ ID NO:32
- 30) SEQ ID NO:33
- 30) SEQ ID NO:34
- 31) SEQ ID NO:35
- 32) SEQ ID NO:36
- 33) SEQ ID NO:37

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- 34) SEQ ID NO:38
- 35) SEQ ID NO:39
- 36) SEQ ID NO:40
- 37) SEQ ID NO:41
- 38) SEQ ID NO:42
- 39) SEQ ID NO:43
- 40) SEQ ID NO:44
- 41) SEQ ID NO:45
- 42) SEQ ID NO:46
- 43) SEQ ID NO:47
- 44) SEQ ID NO:48
- 45) SEQ ID NO:49
- 46) SEQ ID NO:50
- 47) SEQ ID NO:51
- 48) SEQ ID NO:52
- 49) SEQ ID NO:53
- 50) SEQ ID NO:54
- 51) SEQ ID NO:55
- 52) SEQ ID NO:56 or,
- 53) SEQ ID NO:57.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 141 encompasses species 1-53, claim 142 encompasses species 42, 23, 30 and 24 and 37, claim 143 encompasses species 23 and 37, and claim 144 encompasses species 21, 22, 23 and 24. Claims 141, 142, 143 and 144 are generic, for example.

This application contains claims directed to the following species of Group XIX, drawn to a method of treating an autoimmune disease which comprises administering an therapeutically effective amount of an isolated copeptide. If Group XIX is elected, then a species election is required from the following actions of the isolated copeptide;

- 1)inhibits activation of T cells,
- 2)activate T cell mechanisms,
- 3)inhibits activation of T cells specific to myelin basic protein, or
- 4) inhibits activation of T cells specific to collagen type II peptide.

These species are different methods requiring different process steps and/or endpoints.

The claims are deemed to correspond to the species listed above in the following manner: Claim 145 encompasses species 1, claim 146 encompasses species 2, claim 147 encompasses species 3, and claim 148 encompasses species 4. Claims 145-148 are generic, for example.

This application contains claims directed to the following species of Group XIX, drawn to a method of treating an autoimmune disease which comprises administering an therapeutically effective amount of an isolated copeptide that binds to an MHC Class II protein. If Group XIX is elected, then a species election is required from the following MHC ClassII proteins,

- 1) HLA-DR1,
- 2) HLA-DR2, or
- 3) HLA-DR4.

The claims are deemed to correspond to the species listed above in the following manner: Claim 150 encompasses species 1, Claim 151 encompasses species 2, and Claim 152 encompasses species 3.

These species are distinct with respect to their structure and functional characteristics, a person of ordinary skill in the art would not envision one in view of the other. They therefore appear to be separate and species in view of each other.

This application contains claims directed to the following species of Group XIX, drawn to a method of treating an autoimmune disease which comprises administering an therapeutically effective amount of an isolated copeptide that binds to an MHC Class II protein. If Group XIX is elected, then a species election is required from the following autoimmune diseases;

- 1)an arthritic condition,
- 2)a demyelinating disease,
- 3) an inflammatory disease,
- 4)multiple sclerosis,
- 5) autoimmune hemolytic anemia,

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- 6) autoimmune oophoritis,
- 7) autoimmune thyroiditis,
- 8) autoimmune uveoretinitis,
- 9) chronic immune thrombocytopenic purpura,
- 10) colitis,
- 11) contact sensitivity disease,
- 12) diabetes mellitus,
- 13) Guillain-Barre's Disease,
- 14) Hashimoto's Disease,
- 15) idiopathic myxedema,
- 16) idiopathic myxedema,
- 17) myasthenia gravis,
- 18) psoriasis,
- 19) pemphigus vulgaris,
- 20) rheumatoid arthritis, or
- 21) systemic lupus erythematosus.

These species are distinct because the pathological conditions differ in etiologies and therapeutic endpoints.
Claim 154 encompasses species 1-21, and is generic, for example.

Group XX, claim(s) 155, drawn to an isolated nucleic acid encoding copeptides,

This application contains claims directed to the following species of Group XX, drawn to an isolated nucleic acid encoding copeptides. If Group XX is elected, then a species election is required from the following isolated copeptides:

- 1) SEQ ID NO:4
- 2) SEQ ID NO:5
- 3) SEQ ID NO:6
- 4) SEQ ID NO:7
- 5) SEQ ID NO:8
- 6) SEQ ID NO:9
- 7) SEQ ID NO:10
- 8) SEQ ID NO:11
- 9) SEQ ID NO:12
- 10) SEQ ID NO:13
- 11) SEQ ID NO:14
- 12) SEQ ID NO:15
- 13) SEQ ID NO:16
- 14) SEQ ID NO:17
- 15) SEQ ID NO:18
- 16) SEQ ID NO:19
- 17) SEQ ID NO:20
- 18) SEQ ID NO:21
- 19) SEQ ID NO:22
- 20) SEQ ID NO:23
- 21) SEQ ID NO:24
- 22) SEQ ID NO:25
- 23) SEQ ID NO:26
- 24) SEQ ID NO:27
- 25) SEQ ID NO:28
- 26) SEQ ID NO:29
- 27) SEQ ID NO:30
- 28) SEQ ID NO:31
- 29) SEQ ID NO:32
- 30) SEQ ID NO:33
- 30) SEQ ID NO:34
- 31) SEQ ID NO:35
- 32) SEQ ID NO:36
- 33) SEQ ID NO:37
- 34) SEQ ID NO:38
- 35) SEQ ID NO:39

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- 36) SEQ ID NO:40
- 37) SEQ ID NO:41
- 38) SEQ ID NO:42
- 39) SEQ ID NO:43
- 40) SEQ ID NO:44
- 41) SEQ ID NO:45
- 42) SEQ ID NO:46
- 43) SEQ ID NO:47
- 44) SEQ ID NO:48
- 45) SEQ ID NO:49
- 46) SEQ ID NO:50
- 47) SEQ ID NO:51
- 48) SEQ ID NO:52
- 49) SEQ ID NO:53
- 50) SEQ ID NO:54
- 51) SEQ ID NO:55
- 52) SEQ ID NO:56 or,
- 53) SEQ ID NO:57.

These species are distinct with respect to their sequence, a person of ordinary skill in the art would not envision one in view of the other.

The claims are deemed to correspond to the species listed above in the following manner: Claim 155 encompasses species 1-53, and is generic, for example.